

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 01:44:06 ; Search time 2114 Seconds

(without alignments)
10333.841 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534
Sequence: 1 gtcccaatctgaagtgaag.....aaaaaaaaaaaaaaaaaaaaa 534Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	518.4	97.1	530	9	AF096895	AF096895 Homo sapi
2	493.4	92.4	515	6	AR306550	AR306550 Sequence
3	493.4	92.4	515	6	AX061624	AX061624 Sequence
4	466.8	87.4	500	6	BD085905	BD085905 Elongatio
5	465.8	87.2	526	6	AR275027	AR275027 Sequence
6	411.4	77.0	413	6	BD085952	BD085952 Elongatio
7	405.4	75.9	415	6	BD023892	BD023892 Sequence
8	349.4	65.4	689	9	AF145216	AF145216 Homo sapi
9	349	65.4	593	9	AF145216	AF145216 Homo sapi
10	338	63.3	688	9	BC004380	BC004380 Homo sapi
11	325.4	60.9	655	9	AF057306	AF057306 Homo sapi
12	321.8	60.3	669	6	AR306591	AR306591 Sequence
13	321.8	60.3	669	6	AX061665	AX061665 Sequence
14	316.4	59.3	434	9	AF135381	AF135381 Homo sapi
15	278	52.1	485	11	G30204	G30204 human STS S
16	214.4	40.1	59554	6	AX695587	AX695587 Sequence
17	214.4	40.1	97075	9	AC010289	AC010289 Homo sapi
18	214.4	40.1	151620	2	AC018589	AC018589 Homo sapi
19	214.4	40.1	188460	9	AC010542	AC010542 Homo sapi
20	214	40.1	269	6	BD030595	BD030595 Sequence
21	210.2	39.4	321	6	BD139357	BD139357 Extended
22	205	38.4	207	6	AX330610	AX330610 Sequence
23	205	38.4	207	6	AX330787	AX330787 Sequence
24	205	38.4	207	6	AX331008	AX331008 Sequence
25	205	38.4	207	6	AX408097	AX408097 Sequence
26	185.2	34.7	495	6	AX079435	AX079435 Sequence
27	184.8	34.6	180702	9	AC018557	AC018557 Homo sapi
28	165.4	31.0	523	10	AF253064	AF253064 Rattus no
29	158.4	29.7	6283	6	AX252053	AX252053 Sequence
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31	158.4	29.7	6283	6	AX348836	AX348836 Sequence
32	135	25.3	568	10	AY047360	AY047360 Mus muscu
33	126	23.6	682	10	AF253065	AF253065 Rattus no
34	119.4	22.4	6283	6	AX252052	AX252052 Sequence
35	119.4	22.4	6283	6	AX344430	AX344430 Sequence
36	119.4	22.4	6283	6	AX348835	AX348835 Sequence
37	78.4	14.7	45256	9	AC000090	AC000090 Homo sapi
38	73.4	13.7	137334	10	AC121952	AC121952 Mus muscu
39	73.4	13.7	171595	2	AC121275	AC121275 Mus muscu
40	73.4	13.7	209366	2	AC128918	AC128918 Rattus no
41	73.4	13.7	213593	2	AC131402	AC131402 Rattus no
42	73.4	13.7	273571	2	AC112851	AC112851 Rattus no
43	71.2	13.3	682	10	AF401531	AF401531 Mus muscu
44	70.2	13.1	189981	2	AC137048	AC137048 Rattus no
45	70.2	13.1	213593	2	AC131402	AC131402 Rattus no

ALIGNMENTS

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RESULT 1
AF096895 530 bp mRNA linear PRI 18-JUL-2001
LOCUS Homo sapiens chemokine-like factor 1 (CKLP1) mRNA, complete cds.
DEFINITION AF096895
ACCESSION AF096895
VERSION AF096895.2 GI:9989691
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 530)
AUTHORS Han,W., Lou,Y., Tang,J., Zhang,Y., Chen,Y., Li,Y., Gu,W., Huang,J.,
Gul,L., Tang,Y., Li,F., Song,Q., Di,C., Wang,L., Shi,Q., Sun,R.,
Xia,D., Rui,M., Tang,J. and Ma,D.
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TITLE	Molecular cloning and characterization of chemokine-like factor 1 (CKLF1), a novel human cytokine with unique structure and potential chemotactic activity
JOURNAL	Biochem. J. 357 (Pt 1), 127-135 (2001)
MEDLINE	21308461
PUBMED	11415443
REFERENCE	2 (bases 1 to 530)
AUTHORS	Han,W.L., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L.
TITLE	Direct Submission
REFERENCE	Submitted (03-Oct-1998) Immunology, Beijing Medical University, 38 Xue Yuan Rd., Beijing 100083, China
AUTHORS	3 (bases 1 to 530)
REFERENCE	Han,W.L.
TITLE	Direct Submission
REFERENCE	Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK	Sequence update by submitter
COMMENT	On Sep 7, 2000 this sequence version replaced gi:6288733.
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	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/cell_line="U937"
	/note="exposed to phytohaemagglutinin (PHA)"
gene	1..530
	/gene="CKLF1"
	/note="synonym: UCK-1"
CDS	148..447
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	/note="increased expression in PHA stimulated cells; expression inhibited by IL-10"
	/codon_start=1
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	/protein_id="AAF06722.1"
	/db_xref="GI:6288734"
	/translation="MDNVQPKIKRPFCSYKGVKMLRLDIINSLVTVEMLIVSVLA ALIEETTLVTGGGVPFLVTAVCCILADALLIRLLNFPSPRYKKPVRHEKEVL"
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Best Local Similarity	99.8%; Pred. NO. 5.5e-116;
Matches 519; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	15 GTGAAGCCGAGCTGGCGCAAGAATGAGGAGGCGGTCTCCGCCGCGTGCCTTGTCT 74
Db	11 GGGAAGCCGAACTGGCGCAGAAATGAGGAGGCGGTCTCCGCCGCGTGCCTTGTCT 70
Oy	75 ATCGCTTGCAAGAACCTACTACGAGCAGCAGCTGAGAAGATTGAGGAAAATGCTGCTG 134
Db	71 ATCGCTTGCAAGAACCTACTACGAGCAGCAGCTGAGAAGATTGAGGAAAATGCTGCTG 130
Oy	135 CTGGGCTTCGACAGCGCATGTGATAACGTGACGCCGAAAAATAAACATGCCCTTTGCT 194
Db	131 CTGGGCTTCGACAGCGCATGTGATAACGTGACGCCGAAAAATAAACATGCCCTTTGCT 190
Oy	195 TCAGTGTAAAGGCCACGCTGAAGATCGCGCTGGATTAATACAATCACTGGTAACAA 254
Db	191 TCAGTGTAAAGGCCACGCTGAAGATCGCGCTGGATTAATACAATCACTGGTAACAA 250
Oy	255 CAGTATTGATCTCATCTATCTGTGTGGCACTGATACGAAAAACCAACATTTGACAG 314
Db	251 CAGTATTGATCTCATCTATCTGTGTGGCACTGATACGAAAAACCAACATTTGACAG 310
Oy	315 TTGGTGAAGGGGTGTTTSCACTTGTGACAGCAGTATGCTGTCTTGGCGAGCGGGCCCTTA 374
Db	311 TTGGTGAAGGGGTGTTTSCACTTGTGACAGCAGTATGCTGTCTTGGCGAGCGGGCCCTTA 370
Oy	375 TTTTACCGGAAGCTTTCTTTCAATCCCACCGGCTCTTACCAGAAAAAGCTGTGCATGAA 434
Db	371 TTTTACCGGAAGCTTTCTTTCAATCCCACCGGCTCTTACCAGAAAAAGCTGTGCATGAA 430

LOCUS	AX061624	515 bp	DNA	linear	PAT 12-JUN-2003
RESULT 2	AR306550	515 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	AR306550	515 bp	DNA	linear	PAT 12-JUN-2003
DEFINITION	Sequence 29 from patent US 6548633.				
ACCESSION	AR306550				
VERSION	AR306550.1				
KEYWORDS	GI:31696619				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 515)				
AUTHORS	Edwards, J., B. D. M., Bougueleret, L. and Jobert, S.				
TITLE	Complementary DNA's encoding proteins with signal peptides				
JOURNAL	Patent: US 6548633-A 29 15-APR-2003;				
FEATURES	location/Qualifiers				
source	1..515				
BASE COUNT	143 a 106 c 135 g 130 t 1 others				
ORIGIN					
Query Match	92.4%; Score 493.4; DB 6; Length 515;				
Best Local Similarity	99.4%; Pred. No. 7e-110;				
Matches	505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;				
QY	15 GTGAAGCCGAGCTGGCGAGAAAGTAGGAGAGGCGGTCTCCGCCGGTGGCGGTTGCT 74				
DB	8 GGGAAAGCCGAGCTGGCGAGAAAGTAGGAGAGGCGGTCTCG-CGGGTGGCGGTTGCT 66				
QY	75 ATCGCTTGCAGAACTTACTAGCGAGCCAGCTGAGAAAGTTGAGGAAAGTCTGCTG 134				
DB	67 ATCCCTTCGCGAAACCTACTCAGCGACGACCTAGAAAGTTGAGGAAAGTCTGCTG 126				
QY	135 CTGGGCTCGCAGAGCGCGATGGATTAACGTGACGCGGAAATPAAACATCGCCCTTCTGCT 194				
DB	127 CTGGGCTCGCAGAGCGCGATGGATTAACGTGACGCGGAAATPAAACATCGCCCTTCTGCT 186				
QY	195 TCAGTGTGAAGAGCCAGCTGAAGATGCTGCGGCTGATATTATCACTCACTGTGTAA 254				
DB	187 TCAGTGTGAAGAGCCAGCTGAAGATGCTGCGGCTGATATTATCACTCACTGTGTAA 246				
QY	255 CAGTATTCATCTCATGTGATCTGTGTGGTGGCATGTGATCCAGAAACCAACAACTTGACAG 314				
DB	247 CAGTATTCATCTCATGTGATCTGTGTGGTGGCATGTGATCCAGAAACCAACAACTTGACAG 306				
QY	315 TTGGTGAAGGGGGTCTTTTGCATCTTGAGACAGAGATGCTGTTCGCGAGCGGGCCCTTA 374				
DB	307 TTGGTGAAGGGGGTCTTTTGCATCTTGAGACAGAGATGCTGTTCGCGAGCGGGCCCTTA 366				
QY	375 TTTCACCGGAAGCTTCTGTTCAATCCACGCGGCTCCTTACAGAAAAAAGCTGTGCATGAA 434				
DB	367 TTTCACCGGAAGCTTCTGTTCAATCCACGCGGCTCCTTACAGAAAAAAGCTGTGCATGAA 426				
QY	435 AAAAAGAAAGTTTGTAAATTATTAATTAATTGTTGATCTGAAGTATTAACATATT 494				
DB	427 AAAAAGAAAGTTTGTAAATTATTAATTAATTGTTGATCTGAAGTATTAACATATT 486				
QY	495 TCTGTATTCTTCCAAAAAATTTTATTTT 522				
DB	487 TCTGTATTCTTCCAAAAAATTTTATTTT 514				
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LOCUS	AX061624	515 bp	DNA	linear	PAT 24-JAN-2001

DEFINITION Sequence 29 from Patent WO0100806.
ACCESSION AX061624
VERSION AX061624.1 GI:12406709
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1
AUTHORS Dumais mlne Edwards J.B., Bougueleret L. and Jobert S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 29 04-JAN-2001;
GENSET (FR)

FEATURES
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1. 515
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
144. 443
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC24985.1"
/db_xref="GI:12406710"
/translation="MDNVQPKIKHREPCSVKGVKMLRIDIIINSLVTVEMLIIVSL
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144. 287
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/note="Von Heijne matrix score 4.10 seq VFMLIVSVLALIP/ET"
polya_signal 457. 462
polya_site 500. 515
BASE COUNT 143 a 106 c 135 g 130 t 1 others
ORIGIN

Query Match 92.4%; Score 493.4; DB 6; Length 515;
Best Local Similarity 99.4%; Pred. No. 7e-110; Indels 1; Gaps 1;
Matches 505; Conservative 0; Mismatches 2;

15 GTGAAGCCGAGCTGGCGAGAGTAGGGAGGGGGTCTCCGCCGCGTGGCGTCT 74
8 GGGAGCCGAGCTGGCGAGAGTAGGGAGGGGGTCTCCG-CGGCGTGGCGTCT 66
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435 AAAAAGAGTTTGTAAATTTATATTAATTTTATTTTATTTTATTTTAAATTT 494
427 AAAAAGAGTTTGTAAATTTATATTAATTTTATTTTATTTTATTTTAAATTT 486
495 TCTGTATTTCTTCAAAAAAAAAAAAAA 522
487 TCTGTATTTCTTCAAAAAAAAAAAAAA 514

RESULT 4
LOCUS BD085905 500 bp DNA linear PAT 27-AUG-2002
DEFINITION Elongation CDNA of secretory protein.
ACCESSION BD085905
VERSION BD085905.1 GI:22631515
KEYWORDS JP 2001523453-A/47.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1
AUTHORS Bougueleret L., Duclet A. and Edwards J.B.D.M.
TITLE Elongation CDNA of secretory protein
JOURNAL Patent: JP 2001523453-A 47 27-NOV-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001523453-A/47
PD 27-NOV-2001
PR 13-NOV-1998 JP 2000521191 60/066957 PR
PR 13-NOV-1997 US 60/066677,17-DEC-1997 US 60/081563 PR
09-FEB-1998 US 60/074121,13-APR-1998 US 60/099273 PI
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PI
BOUGUELERET,AMERIC DUCLETT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Von Heijne matrix
CC score 5.5899990463257
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2 GAGCTGTNNCNSAAGTAGGGGAGGGCGGTCTCCCGMCGGTGGCGGHTGCTATCGCTT	61	
82 CGCAGAACCTCTCTCAGGAGCGAGCTGAGAGAGTTGAGGGGAAATGCGTGCCTGGCGGTC	141	
62 CGCAGAACCTTACTTCGGCAGCCAGCTTGAGAGAGTTGAGGGGAAATGCTGCTCGGGTC	121	
142 TGCAGACCGATGATGATTAACGTGACGCCGAAATATAAATCACTGCCCCCTTCTGCTTCAGTGT	201	
122 TGCAGACCGATGATGATTAACGTGACGCCGAAATATAAATCACTGCCCCCTTCTGCTTCAGTGT	181	
202 GAAAGGCCACGTGA-AGATGCTGGCGGCTGGATTTATCACTCACTGTTGTAACAACAGTAT	260	
182 GAAAGGCCACGTGAAGATGCTGGCGGCTGGATTTATCACTCACTGTTGTAACAACAGTAT	241	
261 TCATGCTCATGCTATCTGTGTTGGACGTGATCCAGAAACCAACACATTTGACAGTTGGTG	320	
242 TCATGCTCATGCTATCTGTGTTGGACGTGATCCAGAAACCAACACATTTGACAGTTGGTG	301	

QY	321	AAGGGGAGTGTTCGACCTTGTCAGACAGATAGCTGTCTTGCCGACGGGGGCCCTTATTAC	380
Db	302	GAGGGGGGTTCGACCTTGTGAACAGAGTATGCTGTTCGCCACGGGCCCTTATTAC	361
QY	381	GGAAGCTTCTGTCATCCGACGGTCTTACCGAAGAAAGCCTGTGCATGAAAAAAG	440
Db	362	GGAAGCTTCTGTCATCCGACGGTCTTACCGAAGAAAGCCTGTGCATGAAAAAAG	421
QY	441	AAGTTTGTAAATTATTAATTACTTTTATGTTTGTACTTAAGTATTAACATATTTCTGTA	500
Db	422	AAGTTTGTAAATTATTAATTACTTTTATGTTTGTACTTAAGTATTAACATATTTCTGTA	481
QY	501	TTCTTCCAAAAAAGAAAAA 519	
Db	482	TTCTTCCAAAAAAGAAAAA 500	
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LOCUS	Sequence 164 from patent US 6506607.		
DEFINITION	AR275027		
ACCESSION	AR275027.1		
VERSION	GI:29707577		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 526)		
TITLE	Shyjan,A.W.		
JOURNAL	Methods and compositions for the identification and assessment of		
FEATURES	prostate cancer therapies and the diagnosis of prostate cancer		
source	Patent: US 6506607-A 164 14-JAN-2003;		
	Location/Qualifiers		
	1..526		
	/organism="unknown"		
BASE COUNT	133 a 136 c 113 g 143 t	1 others	
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Query Match	87.2%; Score 465.8; DB 6; Length 526;		
Best Local Similarity	99.0%; Pred. No. 3.9e-103;		
Matches	489; Conservative 0; Mismatches 3; Indels 2; Gaps 2		
QY	28	GGGCGAAGTAAGGGGAGGGCGGTGCTCCGCCGCGTGGCGGTGCTATCGCTTGCAGA	87
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QY	88	ACCTACTAGGACAGCCAGCTGATGAAGAATGATGAGGGAAGTGTGCTGCGGTGCGAGA	147
Db	434	ACCTACTAGGACAGCCAGCTGATGAAGAATGATGAGGGAAGTGTGCTGCGGTGCGAGA	375
QY	148	CGCGATGATTAACGTGCAGCCGAAATATAACATC-GCCCTTCTGCTTCAGTGTGAAG	206
Db	374	CGCGATGATTAACGTGCAGCCGAAATATAACATGCGCCCTTCTGCTTCAGTGTGAAG	315
QY	207	GCCACGTGAAGATGCTGCGGCTGATATTAATCACTCACTGGTAACAACAGTATTCATGC	266
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QY	267	TCATGTGATCTGTGTGGACCTGATACACAGAAACCAACAATGACATTTGGTGGAGGG	326
Db	254	TCATGTGATCTGTGTGGACCTGATACACAGAAACCAACAATGACATTTGGTGGAGGG	195
QY	327	TGTTTGCACTTGTGACACAGATAGCTGTCTTGCCGACGGGGCCCTTAATTACCGAAGC	386
Db	134	TGTTTGCACTTGTGACACAGATAGCTGTCTTGCCGACGGGGCCCTTAATTACCGAAGC	135
QY	387	TTCTGTTCATCCGACCGGTCTTACCGAAGAAAGCCTGTGCATGAAAAAAGAGTTT	446
Db	134	TTCTGTTCATCCGACCGGTCTTACCGAAGAAAGCCTGTGCATGAAAAAAGAGTTT	75
QY	447	TGTAAATTTAATTAATCTTTTAAAGTTGATTAAGTATTAACATATTTTC-TGTATTTCT	505
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QY 506 CCAAAAAAAAAA 519
Db 14 CCAAAAAAAAAA 1

RESULT 6
BD085952 413 bp DNA linear PAT 27-AUG-2002
LOCUS Elongation CDNA of secretory protein.
DEFINITION BD085952
ACCESSION BD085952.1 GI:22631562
VERSION JP 2001523453-A/94.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE (bases 1 to 413)
Bouguetier, L., Duclet, A. and Edwards, J.B.D.M.
Elongation CDNA of secretory protein
Patent: JP 2001523453-A 94 27-NOV-2001;
JOURNAL GENSET
OS Homo sapiens (human)
PN JP 2001523453-A/94
PD 27-NOV-2001
PR 13-NOV-1998 JP 2000521191
PR 13-NOV-1997 US 60/066677.17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121.13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116.04-SEP-1998 US 60/092723 PI LYDIE
BOUGUETIER, L., DUCLET, A., EDWARDS, J.B.D.M.,
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
vsn Heijne matrix
CC score 4.0999990463257
CC seq VFWLIVSVLALIP/ET
FH Key Location/Qualifiers
FT sig_peptide 46..189
FT polyA_signal 377..382
FT polyA_site 402..413.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 121 a 82 c 95 g 115 t

ORIGIN

Query Match 77.0%; Score 411.4; DB 6; Length 413;
Best Local Similarity 99.8%; Pred. No. 7.2e-90;
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 107 TGAGAGAGTTGAGGAAAGTGTCTGCTGGGCTCTGAGACGGAGATGATACGTGACG 166
Db 1 TGAGAGAGTTGAGGAAAGTGTCTGCTGGGCTCTGAGACGGAGATGATACGTGACG 60

QY 167 CCGAAATAAATCAATCGCCCTTCTGCTCACTGTGAAGGCCACGTGAAGATCTCGG 226
Db 61 CCGAAATAAATCAATCGCCCTTCTGCTCACTGTGAAGGCCACGTGAAGATCTCGG 120

QY 227 CTGATATTTATCACTCACTGATTAACAACAGTATTTCACTGATCTGTGTGTGCA 286
Db 121 CTGATATTTATCACTCACTGATTAACAACAGTATTTCACTGATCTGTGTGTGCA 180

QY 287 CTGATACCAAAACCAACATTTGACAGTTGGTGGAGGGGTGTTGCACTTTGACAGCA 346
Db 181 CTGATACCAAAACCAACATTTGACAGTTGGTGGAGGGGTGTTGCACTTTGACAGCA 240

QY 347 GTATGCTCTTGTGGCGAGGGGGCTTATTTACCGGAAGCTTCTGTTCAATCCAGGGGT 406
Db 241 GTATGCTCTTGTGGCGAGGGGGCTTATTTACCGGAAGCTTCTGTTCAATCCAGGGGT 300

QY 407 CCTTACAGAAAAGCCTGTGATGAAAAAAGAGTTTGTATTTATTTACTTTT 466

Db 301 CCTTACAGAAAAGCCTGTGATGAAAAAAGAGTTTGTATTTATTTACTTTT 360
QY 467 TAGTTGATCTAGTATTAACATATTTCTGATTTCTTCCAAAAA 519
Db 361 TAGTTGATCTAGTATTAACATATTTCTGATTTCTTCCAAAAA 413

RESULT 7
BD023892 415 bp DNA linear PAT 27-AUG-2002
LOCUS Sequence tag and encoded human protein.
DEFINITION BD023892
ACCESSION BD023892.1 GI:22565115
VERSION JP 2001269182-A/138.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE (bases 1 to 415)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Edwards, J.B.D.M., Duclet, R. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 138 02-OCT-2001;
JOURNAL GENSET
OS Homo sapiens (human)
PN JP 2001269182-A/138
PD 02-OCT-2001
PR 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68, G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC score 4.1
CC seq VFWLIVSVLALIP/ET
FH Key Location/Qualifiers
FT CDS 146..415
FT sig_peptide 146..289.
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source Location/Qualifiers
1..415
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 101 a 97 c 126 g 91 t

ORIGIN

Query Match 75.9%; Score 405.4; DB 6; Length 415;
Best Local Similarity 99.8%; Pred. No. 2.1e-88;
Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 GTAAAGCCAGCTGGGCGAGAGTAAAGGAGGCGGTCTCCGCGGTGGCGTTGCT 74
Db 9 GGAAGCCAGCTGGGCGAGAGTAAAGGAGGCGGTCTCCGCGGTGGCGTTGCT 68

QY 75 ATGCGTTCCGAGAACTCACTCAAGCCAGCCAGCGAGAAAGGTGAAGGAAAGGTGCTG 124
Db 69 ATGCGTTCCGAGAACTCACTCAAGCCAGCCAGCGAGAAAGGTGAAGGAAAGGTGCTG 128

QY 135 CTGGGCTGTGAGACGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 194
Db 129 CTGGGCTGTGAGACGGATGATGATGATGATGATGATGATGATGATGATGATGAT 188

QY 195 TCAAGTGAAGGCGACGTGAAGATGCTGCGCTGTGATTTATCACTCACTGTTAA 254
Db 189 TCAAGTGAAGGCGACGTGAAGATGCTGCGCTGTGATTTATCACTCACTGTTAA 248

QY 255 CAGATTTCACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 314
Db 249 CAGATTTCACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 308

QY 315 TTGGTGAAGGGGTGTTGCACTTTGTCAGACAGATATGCTGCTTGGCGAGGGGCCCTTA 374

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Db 309 TTGGGAGGGGGTCTTTCACCTTGAGACAGAGTAGCTGCTCCAGGGGCGCTTA 368
Oy 375 TTACCGGAGCTTCTGTTCAATCCAGCGGTCTTACAGAAAAAG 421
Db 369 TTACCGGAGCTTCTGTTCAATCCAGCGGTCTTACAGAAAAAG 415

RESULT 8
AF135380 689 bp mRNA linear PRI 07-SEP-2000
LOCUS Homo sapiens chemokine-like factor 2 (CKLF2) mRNA, complete cds.
DEFINITION alternatively spliced.
ACCESSION AF135380
VERSION AF135380.2 GI:9898692
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 689)
Han, W. L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.
Direct Submission
Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
2 (bases 1 to 689)
Han, W. L.
Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK
Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:6630853.
FEATURES
location/Qualifiers
source
1..689
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/notes="from PHA stimulated cells"
1..689
/gene="CKLF2"
/notes="UCK"
148..606
/gene="CKLF2"
/notes="UCK"
/notes="UCK-2; alternatively spliced"
/codon_start=1
/product="chemokine-like factor 2"
/protein_id="AAFI8599.1"
/db_xref="GI:6630854"
/translation="MDNVQPKIKRPFCSYKGVKMLRLALVTSTMTFFIIAQAPR
YIVITGEVIVILFEILYVLRDLRMKMLFPLDILINSIVTTFMILISVLAIPR
TTTLVGGGVFALVTAVCCCLADGALIRKLLFNDSGPYQKKPVHEKKEV."
BASE COUNT 195 a 140 c 161 g 193 t
ORIGIN
Query Match 65.4%; Score 349.4; DB 9; Length 689;
Best Local Similarity 76.4%; Pred. No. 1,1e-74;
Matches 519; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

Oy 15 GTGAAGCCGAGCTGGCGAGAAAGTAGGGAGGCGGTCTCCGCCGTGGCGGTGCT 74
Db 11 GGGAAGCCGAGCTGGCGAGAAAGTAGGGAGGCGGTCTCCGCCGTGGCGGTGCT 70
Oy 75 ATCGCTTGCGAGAACTCTCAGGAGCGCAGCTGAGAGAGTTGAGGGAAGTGTGCTG 134
Db 71 ATCGCTTGCGAGAACTCTCAGGAGCGCAGCTGAGAGAGTTGAGGGAAGTGTGCTG 130
Oy 135 CTGGGTCTGACAGCGCAGTAGATACTGACAGCGGAAATATTAATCGCCCTTCTGCT 194
Db 131 CTGGGTCTGACAGCGCAGTAGATACTGACAGCGGAAATATTAATCGCCCTTCTGCT 190
Oy 195 TCAGTGAAGGCGCAGTAGAAGTGTGCGGCTG----- 229

Db 191 TCAGTGAAGGCGCAGTAGAAGTGTGCGGCTGCGACTTAAGTGCATCTATGACCT 250
Oy 230 ----- 229
Db 251 TTTTATCATCGACAAGCCCTGAACATATATTTGATCACTGATTTGAATCACCG 310
Oy 230 ----- 229
Db 311 TTAATCTATTTTCATACCTTTATATGACTCAGACTGATGCATTAATGAAGTGTAT 370
Oy 230 -----GATATATCAACTCACTGTAACAACAGATTTCATGCTAT 275
Db 371 TTGGCCTTCTGTTGATTTATCACTCACTGTAACAAGATTTCATGCTAT 430
Oy 276 CTGTGTGGCAGTATACAGAAACCAACATTCAGTGTGAGGGGTGTTGCAC 335
Db 431 CTGTGTGGCAGTATACAGAAACCAACATTCAGTGTGAGGGGTGTTGCAC 490
Oy 336 TTGTGACAGAGTAGTGTCTGTCGCGAGCGGGCCCTTATTACCGGAAGCTTGTGCA 395
Db 491 TTGTGACAGAGTAGTGTCTGTCGCGAGCGGGCCCTTATTACCGGAAGCTTGTGCA 550
Oy 396 ATCCAGCGGTCTTACAGAAAGCGTGTGATGAAAAAGAGTTTGTAAATTT 455
Db 551 ATCCAGCGGTCTTACAGAAAGCGTGTGATGAAAAAGAGTTTGTAAATTT 610
Oy 456 ATATTACTTTTATGTTGATCTAGTATTAACATATTTCTGTATTTTCCAAAAAA 515
Db 611 ATATTACTTTTATGTTGATCTAGTATTAACATATTTCTGTATTTTCCAAAAAA 670
Oy 516 AAAAAAAAAAAAAAAAAA 534
Db 671 AAAAAAAAAAAAAAAAAA 689

RESULT 9
AF145216 593 bp mRNA linear PRI 07-SEP-2000
LOCUS Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF145216
VERSION AF145216.2 GI:9898694
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 593)
Han, W. L., Gu, W. F., Li, Y., Zhang, Y. M., Di, C. H., Song, Q. S. and
Ma, D. L.
Direct Submission
Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
2 (bases 1 to 593)
Han, W. L.
Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK
Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:6625671.
FEATURES
location/Qualifiers
source
1..593
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/notes="from PHA stimulated cells"
1..593
/gene="CKLF4"
/notes="synonym: UCK"
148..510
/gene="CKLF4"
/notes="UCK-4; alternatively spliced"
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Db 373 TGAATATCAACTCACTGTGTAACAAGATTTATCATCTCATCTGATCTGTGGCACT 432
Qy 289 GATACCGAAGAACCAATCATTTGACAGTGTGGAGGGGGTGTTCACATTTGACAGAGT 348
Db 433 GATACCGAAGAACCAATCATTTGACAGTGTGGAGGGGGTGTTCACATTTGACAGAGT 492
Qy 349 ATGCTGCTTGGCCAGCGGGCCCTTATTATACCGAAGCTTCTGTTCAATCCAGCGGTCC 408
Db 493 ATGCTGCTTGGCCAGCGGGCCCTTATTATACCGAAGCTTCTGTTCAATCCAGCGGTCC 552
Qy 409 TTACAGAAAAAGCTGTGATGAAAAAAGAAAGTTTGTATTATTAATCTTTTA 468
Db 553 TTACAGAAAAAGCTGTGATGAAAAAAGAAAGTTTGTATTATTAATCTTTTA 612
Qy 469 GTTGTATCTAAGTATTAACATTTCTGATCTTCCAAAAAATTTTATTTTAA 528
Db 613 GTTGTATCTAAGTATTAACATTTCTGATCTTCCAAAAAATTTTATTTTAA 672
Qy 529 AAAAAA 534
Db 673 AAAAAA 678
RESULT 11
AF057306 655 bp mRNA linear PRI 31-DEC-1999
LOCUS Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.
DEFINITION AF057306
ACCESSION AF057306
VERSION AF057306.1 GI:6648618
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 655)
AUTHORS Zhang,J.S., Nelson,M., Wang,L. and Smith D.I.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic and Foundation, Rochester, MN 55905, USA
FEATURES
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/db_xref="taxon:9606"
/cell_line="A5PC-1"
/tissue_type="pancreas"
/note="adenocarcinoma"
1..655
/gene="C32"
132..590
/gene="C32"
/note="down regulated upon cell differentiation induced by sodium butyrate"
/codon_start=1
/product="transmembrane proteolipid"
/protein_id="AA021255.1"
/db_xref="GI:6648618"
/translation="MDNVQPKIKRPFCSVKGVKMKRLALVTSTNPTFIQADEP
YVITGEVTVLFFLLVLRDLRMKMLFWPLLDIINSLVTVMLIVSVALTPE
TTTLVGGGFALVTAVCCADALALYRKLFLNPSGYPQKRPVHEKEVL"
BASE COUNT 171 a 137 c 153 g 194 t
ORIGIN
Query Match 60.9%; Score 325.4; DB 9; Length 655;
Best Local Similarity 75.6%; Pred. No. 7,7e-69;
Matches 495; Conservative 0; Mismatches 1; Indels 159; Gaps 1;
Qy 21 CCGAGCTGGCGGAGAACTAGGGAGGGCGTCCCGCGCGGTGGCGGTTCATCGCT 80
Db 1 CCGAGCTGGCGGAGAACTAGGGAGGGCGGTCCCGCGCGGTGGCGGTTCATCGCT 60
Qy 81 TCCGAGAACTACTCAGGAGCCAGCTGAGAAAGATTGAGGAAAGTGTGCTGGGT 140

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Db 61 TCCGAGAACTACTCAGGAGCCAGCTGAGAAAGATTGAGGAAAGTGTGCTGGGT 120
Qy 141 CTGCAAGCGAGATGATTAACGTGACCGCAAAATAAACATGCGCCCTCTGTCAGTG 200
Db 121 CTGCAAGCGAGATGATTAACGTGACCGCAAAATAAACATGCGCCCTCTGTCAGTG 180
Qy 201 TGAAGGCCACGTGAAGATGCTGCGGCTG----- 229
Db 181 TGAAGGCCACGTGAAGATGCTGCGGCTGCACTACTGACATCTATGACCTTTTAA 240
Qy 230 ----- 229
Db 241 TCATCCACAAGCCCTGAACCATATATGTTATCATCTGGAATTTGAAGTACCGTATCT 300
Qy 230 ----- 229
Db 301 TATTTTCACTTTTATATGTAATGTAACACTGATGATTAATGAAGTGTTATTTGGC 360
Qy 230 -----GATAATTATCACTGATGTAACAAAGTATTCATCTGATCTGTGT 281
Db 361 CTTTGCTGATATTAATCACTGATGTAACAAAGTATTCATCTGATCTGTGT 420
Qy 282 TGGCACTGATACCAAGAACCAACATTTGACAGTGTGAGGGGCTTTGCACTTGTGA 341
Db 421 TGGCACTGATACCAAGAACCAACATTTGACAGTGTGAGGGGCTTTGCACTTGTGA 480
Qy 342 CAGCACTAAGCTGTCTGGCGACGGGGCCCTTATTAACCGGAAGCTTCTGTTCAATCCA 401
Db 481 CAGCACTAAGCTGTCTGGCGACGGGGCCCTTATTAACCGGAAGCTTCTGTTCAATCCA 540
Qy 402 GCGGCTCTTACCGAAGAACCTGTGATGAAAAAAGAAAGTTTGTATTATTAATTA 461
Db 541 GCGGCTCTTACCGAAGAACCTGTGATGAAAAAAGAAAGTTTGTATTATTAATTA 600
Qy 462 CTTTGTAGTTGATTAAGTATTAACATATTCTGTATTTCTTCCAAAAA 516
Db 601 CTTTGTAGTTGATTAAGTATTAACATATTCTGTATTTCTTCCAAAAA 655
RESULT 12
AR306591 669 bp DNA linear PAT 12-JUN-2003
LOCUS AR306591
DEFINITION Sequence 70 from patent US 6548633.
ACCESSION AR306591
VERSION AR306591.1 GI:31696660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 669)
AUTHORS Edwards,J.-B.D.M., Bougueleret,L. and Jobert,S.
TITLE Complementary DNA's encoding proteins with signal peptides
JOURNAL Patent: US 6548633-A 70 15-APR-2003;
FEATURES
source
1..669
/organism="unknown"
BASE COUNT 178 a 139 c 158 g 194 t
ORIGIN
Query Match 60.3%; Score 321.8; DB 6; Length 669;
Best Local Similarity 75.6%; Pred. No. 5,9e-68;
Matches 504; Conservative 0; Mismatches 2; Indels 161; Gaps 2;
Qy 15 GTGAGCCCAAGCTGGCGGAGAGTAGGGAGGGCGGTCTCGCGCGGTGGCGGTGCT 74
Db 5 GGGAGCCCAAGCTGGCGGAGAGTAGGGAGGGCGGTCTCGCGCGGTGGCGGTGCT 64
Qy 75 ATGCGTTCGCAAGAACTACTCAGGAGCCAGCTGAGAAAGTTGAGGAAAGTGTGCTG 134
Db 65 ATGCGTTCGCAAGAACTACTCAGGAGCCAGCTGAGAAAGTTGAGGAG--ATTGCTGCTG 122
Qy 135 CTGGGCTCGCAGACCGGATGATTAACGTGACGCCGAAAAATCAATCCGCCCTTCTGCT 194

Db 123 CTGGGCTGAGACGGATGATTAACGTGACGCGAAATTAACATGCGCCCTTCTGCT 182
QY 195 TCAGTGGAAAGGCCACGTGAAGATGCTGGGCTG----- 229
Db 183 TCAGTGGAAAGGCCACGTGAAGATGCTGGGCTGGACACTAATCTATGACCT 242
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Db 303 TTATCTTATTTTTCATCTTTTATATGACTCAAGCTTGATTCGATTAATGAGTGTAT 362
QY 230 -----GATTTATCAACTCAGTGGTAAACAGATTTGATGTCATGCTAT 275
Db 363 TTTGGCCTTGGCTGATATATATCAACTCACTGGTAAACAGATTTATCATGCTAT 422
QY 276 CTGTGTTGGACATGATACCAAGAACCAACATTGACAGTTGTGAGGGGTGTTGCAC 335
Db 423 CTGTGTTGGACATGATACCAAGAACCAACATTGACAGTTGTGAGGGGTGTTGCAC 482
QY 336 TTGTGACAGAGTATGCTGCTTCCGACGCGGCGCTTATTTACCGAAGCTTCTGTCA 395
Db 483 TTGTGACAGAGTATGCTGCTTCCGACGCGGCGCTTATTTACCGAAGCTTCTGTCA 542
QY 396 ATCCGACGGCTCTTACCAAGAACCGTGTGCAAGAAAAAGAGTTTGAATTTT 455
Db 543 ATCCGACGGCTCTTACCAAGAACCGTGTGCAAGAAAAAGAGTTTGAATTTT 602
QY 456 ATATTACTTTTATGTTGATAGTATTAACATATTTCTGATTTCTCCAAAAAAA 515
Db 603 ATATTACTTTTATGTTGATAGTATTAACATATTTCTGATTTCTCCAAAAAAA 662
QY 516 AAAAAA 522
Db 663 AAAAAA 669

RESULT 13
LOCUS AX061665 669 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 70 from Patent WO0100806.
ACCESSION AX061665
VERSION AX061665.1 GI:12406789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS dumas milne Edwards,J.B., Bougueleret,L. and Jobert,S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 70 04-JAN-2001;
GENSET (PR)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
140..598
/note="unnamed protein product"
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/db_xref="GI:12406790"
/translation="MDNVQPKIKRPFCSVKGHVKMLRLALVTWSMTFFLIAQAPP
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sig_peptide 140..442
polya_signal /note="Von Heijne matrix score 4.10 seq VPMIVSLALIP/ET"
polya_site 630..635
655..669

BASE COUNT 178 a 139 c 158 g 194 t
ORIGIN
Query Match 60.3%; Score 321.8; DB 6; Length 669;
Best Local Similarity 75.6%; Pred. No. 5,9e-68;
Matches 504; Conservative 0; Mismatches 2; Indels 161; Gaps 2;
QY 15 GTGAAGCCGAGCTGGGCGAAGATAGAGGAGGGGCTGCTCCGCGCGGTGGCTGCT 74
Db 5 GGAAGCCGAGCTGGGCGAAGATAGAGGAGGGGCTGCTCCGCGCGGTGGCTGCT 64
QY 75 ATGCTTTCGAGAACTTACTCAGGCGACGCTGAGAAAGTTGAGGAAAGTCTGCTG 134
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QY 135 CTGGGCTGCGACGCGATGATTAAGTGTGACGCGAAGAAAAATTAACATGCGCCCTTCTGCT 194
Db 123 CTGGGCTGCGACGCGATGATTAAGTGTGACGCGAAGAAAAATTAACATGCGCCCTTCTGCT 182
QY 195 TCAGTGGAAAGGCCACGTGAAGATGCTGGGCTG----- 229
Db 183 TCAGTGGAAAGGCCACGTGAAGATGCTGGGCTGGACACTAATCTATGACCT 242
QY 230 ----- 229
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QY 230 ----- 229
Db 303 TTATCTTATTTTTCATCTTTTATATGACTCAAGCTTGATTCGATTAATGAGTGTAT 362
QY 230 -----GATTTATCAACTCAGTGGTAAACAGATTTGATGTCATGCTAT 275
Db 363 TTTGGCCTTGGCTGATATATATCAACTCACTGGTAAACAGATTTATCATGCTAT 422
QY 276 CTGTGTTGGACATGATACCAAGAACCAACATTGACAGTTGTGAGGGGTGTTGCAC 335
Db 423 CTGTGTTGGACATGATACCAAGAACCAACATTGACAGTTGTGAGGGGTGTTGCAC 482
QY 336 TTGTGACAGAGTATGCTGCTTCCGACGCGGCGCTTATTTACCGAAGCTTCTGTCA 395
Db 483 TTGTGACAGAGTATGCTGCTTCCGACGCGGCGCTTATTTACCGAAGCTTCTGTCA 542
QY 456 ATATTACTTTTATGTTGATAGTATTAACATATTTCTGATTTCTCCAAAAAAA 515
Db 603 ATATTACTTTTATGTTGATAGTATTAACATATTTCTGATTTCTCCAAAAAAA 662
QY 516 AAAAAA 522
Db 663 AAAAAA 669

RESULT 14
LOCUS AF135381 434 bp mRNA linear PRI 07-SEP-2000
DEFINITION Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,
alternatively spliced.
ACCESSION AF135381
VERSION AF135381.2 GI:9989693
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China

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REFERENCE      2 (bases 1 to 434)
AUTHORS       Han, W.L.
TITLE         Direct Submission
JOURNAL       Submitted (07-SEP-2000) Immunology, Peking University Health
              Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK        Sequence update by submitter
COMMENT       On Sep 7, 2000 this sequence version replaced gi:6630855.
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               /note="UCR"
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               /note="UCR-3; alternatively spliced"
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BASE COUNT    127 a      88 c      116 g      103 t
ORIGIN
Query Match   59.3%; Score 316.4; DB 9; Length 434;
Best Local Similarity 81.3%; Pred. No. 1.1e-66;
Matches 423; Conservative 0; Mismatches 1; Indels 96; Gaps 1;

QY 15 GTGAGCGGAGCTGGGGGAGAGTAGGAGGAGGGGCGGCTCCGCGGGGCGGCTGCT 74
DB 11 GGGAGCGGAGCTGGGGGAGAGTAGGAGGAGGGGCGGCTCCGCGGGGCGGCTGCT 70
QY 75 ATCGCTTCGAGAACTTACTCAGCAGCAGCAGCTGAGAAAGATTGAGGAAAGTCTCTG 134
DB 71 ATCGCTTCGAGAACTTACTCAGCAGCAGCAGCTGAGAAAGATTGAGGAAAGTCTCTG 130
QY 135 CTGGGCTCGAGAGCGGATGATTAACGTGACGCCGAAATTAATCATGCCCTTCTGCT 194
DB 131 CTGGGCTCGAGAGCGGATGATTAACGTGACGCCGAAATTAATCATGCCCTTCTGCT 190
QY 195 TCAGTGTGAAGGCGACGTGAAGATCGTGGCGCTGGAATATATCACTCACTGTGTAACA 254
DB 191 TCAGTGTGAAGGCGACGTGAAGATCGTGGCGCT----- 224
QY 255 CAGTATTCATGCTCATGCTATCTGTGTGGACATGATACAGAAACCAACATTGACAG 314
DB 225 ----- 224
QY 315 TTGCTGAGGGGTGTTGCTCACTTGTGACAGCAGATGCTGTCTTCCGACGGGGCCCTTA 374
DB 225 -----GGTGTTCACCTTGTGACAGCAGATGCTGTCTTCCGACGGGGCCCTTA 274
QY 375 TTACCGGAAGCTTCTGTTCAATCCGACGGGTCTTACCAAAAAAGCTGTGATGAAA 434
DB 275 TTACCGGAAGCTTCTGTTCAATCCGACGGGTCTTACCAAAAAAGCTGTGATGAAA 334
QY 435 AAAAAGAAAGTTTGAATTTATTTACTTTTATTTGTTGATTAAGTATTAACATTT 494
DB 335 AAAAAGAAAGTTTGAATTTATTTACTTTTATTTGTTGATTAAGTATTAACATTT 394
QY 495 TCTGTATTCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 534
DB 395 TCTGTATTCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 434

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RESULT 15
G30204/c      G30204      485 bp      DNA      linear      STS 05-OCT-1996
LOCUS

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DEFINITION    human STS SHGC-36487, sequence tagged site.
ACCESSION    G30204
VERSION      G30204.1 GI:1593755
KEYWORDS     STS; STS sequence; primer; sequence tagged site.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 485)
AUTHORS       Myers, R.M.
JOURNAL       Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-314, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: ACTCTTTTTCATGCACAGG
Primer B: GCCCTATTACCGAGACT
STS size: 77
PCR Profile:
  Initial incubation: 94 degrees C for 90 seconds
  Denaturation:      94 degrees C for 15 seconds
  Annealing:         62 degrees C for 23 seconds
  Polymerization:    72 degrees C for 30 seconds
  PCR Cycles:        30
  Thermal Cycler:    Perkin Elmer 9600
  Protocol:
    Template:        25 ng
    Primer:          each 1 uM
    dNTPs:           each 200 uM
    Taq Polymerase:  0.05 units/uL
    Total Vol:       10 uL
  Buffer:
    MgCl2:           2.5 mM
    KCl:             50 mM
    Tris-HCl:        20 mM
    pH:              8.3

Prepared with primer pairs provided by Sandoz, derived from T90569
-- Washington University/Merck EST sequence.

FEATURES
  source       1..485
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /map="16"

STS
  primer_bind  69..145
               complement(126..145)
  primer_bind  146 a      99 c      99 g      131 t      10 others
BASE COUNT    146 a      99 c      99 g      131 t      10 others
ORIGIN
Query Match   52.1%; Score 278; DB 11; Length 485;
Best Local Similarity 97.9%; Pred. No. 2.8e-57;
Matches 281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 226 GGTGATATTATCACTCACTGTAACACAGTATTCATGCTGATGCTATCTGTGTGGC 285
DB 287 GCTTATATTATCACTCACTGTAACACAGTATTCATGCTGATGCTATCTGTGTGGC 228
QY 286 ACTGATACCAAGAACCAACATTTGAGTGTGAGGGGTGTTGCACTTGTGACAGC 345
DB 227 ACTGATACCAAGAACCAACATTTGAGTGTGAGGGGTGTTGCACTTGTGACAGC 168
QY 346 AGTATGCTGTCTTGGCGAGGGGCCCTTATTTTACCGGAAGCTTCTGTCAATCCACGGG 405
DB 167 AGTATGCTGTCTTGGCGAGGGGCCCTTATTTTACCGGAAGCTTCTGTCAATCCACGGG 108

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 01:42:21 ; Search time 250 Seconds
(without alignments)
5766.000 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534
Sequence: 1 gtccccatctgaagtcgaag.....aaaaaaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_19Jun03:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*
26: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	534	100.0	534	21	AAA38006
2	507	94.9	655	22	AA54932
3	498.2	93.3	538	22	AAH98515
4	498.2	93.3	538	22	AAH98548
5	497.2	93.1	558	22	AAH4835
6	493.4	92.4	515	21	AAH87730
7	493.4	92.4	515	22	AAF64012
8	486.6	91.1	504	19	AAV59598

9	486.6	91.1	504	24	AB573585
10	478.6	89.6	506	19	AAV59746
11	478.6	89.6	506	24	AAV57339
12	466.8	87.4	500	20	AAH97826
13	465.4	87.2	467	21	AAH15929
14	425	79.6	439	20	ABK36006
15	411.4	77.0	413	20	AAH97873
16	405.4	75.9	415	21	AAH00147
17	335	62.7	663	20	AA234051
18	335	62.7	663	21	AAH78498
19	335	62.7	663	21	AAH58238
20	335	62.7	663	25	ABX92423
21	327.2	61.3	908	22	AA544933
22	321.8	60.3	669	21	AAH87771
23	321.8	60.3	669	22	AAH45053
24	309.8	58.0	354	20	AAH41509
25	309	57.9	637	21	AA56747
26	306.6	57.4	670	24	ABH90366
27	305.8	57.3	638	24	ABK35884
28	300	56.2	566	22	AAH45120
29	300	56.2	566	22	AAH45121
30	295.4	55.3	297	21	AAH15919
31	285	53.4	544	23	ABV56930
32	272	50.9	382	21	AAH16090
33	224.4	42.0	459	21	AAH8007
34	214.4	40.1	6021	22	AAH82407
35	214.4	40.1	13744	22	AAH68361
36	214.4	40.1	13744	22	AAH82406
37	214	40.1	269	21	AAH06950
38	210.2	39.4	321	20	AAH97651
39	205	38.4	207	24	ABH94246
40	205	38.4	207	24	ABH62782
41	205	38.4	207	24	ABH62959
42	205	38.4	207	24	ABH63180
43	201.4	37.7	326	24	ABO57138
44	185.2	34.7	495	20	AA234052
45	185.2	34.7	495	21	AAH78499

ALIGNMENTS

RESULT 1	AAA38006	standard; cDNA; 534 BP.
XX	AAA38006	
AC	AAA38006	
XX	22-AUG-2000 (first entry)	
DT	22-AUG-2000 (first entry)	
XX	UCC-1 nucleotide sequence.	
XX	UCC-1, chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;	
KW	radiotherapy; Chemotherapy; human; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	CNI244584-A.	
PN	16-FEB-2000.	
PD	16-FEB-2000.	
XX	14-MAY-1999; 99CN-0107284.	
PF	14-MAY-1999; 99CN-0107284.	
XX	14-MAY-1999; 99CN-0107284.	
PR	14-MAY-1999; 99CN-0107284.	
XX	(VYBE-) UNIV BEIJING MEDICAL.	
PA	Ma D, Han W, Zhang Y;	
XX	Ma D, Han W, Zhang Y;	
PI	WPI: 2000-388170/34.	
XX	P-PSDB; AA198142.	
DR	Chemotactic factor useful for treatment and diagnosis of immunocyte	
XX	Chemotactic factor useful for treatment and diagnosis of immunocyte	
PT	Chemotactic factor useful for treatment and diagnosis of immunocyte	

Human cDNA #1 for
Human secreted pro
Human cDNA #2 for
Human secreted pro
Human secreted pro
Human protein clon
cDNA sequence #397
Human secreted pro
Human secreted pro
Human PRO772 nucle
Human PRO772 UNQ4
cDNA encoding huma
cDNA encoding huma
cDNA encoding nove
cDNA encoding pro
cDNA encoding huma
Human secreted pro
Human secreted pro
Human transmembran
Human polynucleoti
cDNA sequence #275
cDNA encoding nove
cDNA encoding nove
Human protein clon
Human prostate exp
Human colon cancer
UCC-2 nucleotide s
Gene #744 used to
Breast cancer rela
Breast cancer rela
Breast cancer rela
Human colon cancer
Human EST DNA33509
Human EST DNA33509

PT disorders - has immunocyte chemotactic stimulating factor
 XX
 PS Example 4; Fig 1; 31pp; Chinese.
 XX
 CC This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis
 CC factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis
 CC activity and a haemopoiesis stimulating effect. The invention relates to
 CC UCK proteins, their encoding nucleotide sequences and antibodies and
 CC antagonists against the proteins. The nucleotide and protein sequences
 CC are useful for the preparation of a composition for the diagnosis and
 CC treatment of diseases associated with abnormal immunocyte function and
 CC low haemopoiesis function caused by radiotherapy and chemotherapy used to
 CC treat tumours and other diseases.
 CC
 XX
 SQ Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;
 Query Match 100.0%; Score 534; DB 21; Length 534;
 Best Local Similarity 100.0%; Pred. No. 2.3e-107;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCCCAATCTGAAGTGAAGCCGAGCTGGGCGAAGTAGGGGAGGGGCTCCGCGC 60
 Db 1 GTTCCCAATCTGAAGTGAAGCCGAGCTGGGCGAAGTAGGGGAGGGGCTCCGCGC 60
 QY 61 CGGTGGCGTGGTCTATCGCTTCGAGAACTTACTCAGGCAAGCCAGCTGAGAGATTGAG 120
 Db 61 CGGTGGCGTGGTCTATCGCTTCGAGAACTTACTCAGGCAAGCCAGCTGAGAGATTGAG 120
 QY 121 GGAAGTGTCTGCTGCTGGGCTTCGAGACGGGATGATGATGATGATGATGATGATGAT 180
 Db 121 GGAAGTGTCTGCTGCTGGGCTTCGAGACGGGATGATGATGATGATGATGATGATGAT 180
 QY 181 TCGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 181 TCGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 CTCAGTGTGAACAACAGTATTCATGCTCATGCTATCTGCTGCTGCTGCTGCTGCTGCT 300
 Db 241 CTCAGTGTGAACAACAGTATTCATGCTCATGCTATCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 301 CACAACATTGACAGTGTGGAGGGGCTGTTGCACTTGTGACAGCAGTATGCTGCTTGC 360
 Db 301 CACAACATTGACAGTGTGGAGGGGCTGTTGCACTTGTGACAGCAGTATGCTGCTTGC 360
 QY 361 CGAGGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGGGGCTTATCCAGAAAA 420
 Db 361 CGAGGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGGGGCTTATCCAGAAAA 420
 QY 421 GCCTGTGCATGAAAAAAGAGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTAT 480
 Db 421 GCCTGTGCATGAAAAAAGAGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTAT 480
 QY 481 GTATTAACATATTTCTGTAATTTCTTCAAAAAAAGAGTTTGTATTTTATTTTATTTTAT 534
 Db 481 GTATTAACATATTTCTGTAATTTCTTCAAAAAAAGAGTTTGTATTTTATTTTATTTTAT 534
 RESULT 2
 AAS44932 standard; cDNA; 655 BP.
 XX
 AC AAS44932;
 XX
 DT 18-DEC-2001 (first entry)
 DE
 XX cDNA encoding novel human secretory protein, Seq ID No 13.
 XX
 KM Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KM ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KM gut protection; lung; liver fibrosis; immune deficiency; infection;

KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KM fertility; analgesic; pain; antigen; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20016689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001MO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 DR WPI; 2001-589934/66.
 DR P-PDB; AAU28032.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 PS Claim 1; SEQ ID No 13; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating disease,
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.
 XX
 SQ Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;
 Query Match 94.9%; Score 507; DB 22; Length 655;
 Best Local Similarity 100.0%; Pred. No. 1.9e-101;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 19 AGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTGCTCCGCCGGTGGCGGTGCTATCG 78
DB 1 AGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTGCTCCGCCGGTGGCGGTGCTATCG 60
QY 79 CTTCGCAAGAACCTTACTTACGACGACGACCTGAGAAAGTTAGAGGAAAGTCTGCTG 138
DB 61 CTTCGCAAGAACCTTACTTACGACGACGACCTGAGAAAGTTAGAGGAAAGTCTGCTG 120
QY 139 GTCTGCAGACGCGATGATGATACGTGACGCGGAAATATAACATCGCCCTTCTGCTCAG 198
DB 121 GTCTGCAGACGCGATGATGATACGTGACGCGGAAATATAACATCGCCCTTCTGCTCAG 180
QY 199 TGTGAAGGCGCAGTGAAGATGCTGCGGCTGATATATATCACTGCTGTAACAACAGT 258
DB 181 TGTGAAGGCGCAGTGAAGATGCTGCGGCTGATATATATCACTGCTGTAACAACAGT 240
QY 259 ATTCAATCTCATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 318
DB 241 ATTCAATCTCATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 319 TGGAGGGGTGTTGCACTTGGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
DB 301 TGGAGGGGTGTTGCACTTGGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 379 CCGGAACTTCTGTTCAATCCAGCGGTCTTACACAGAAAAAGCTGTGATGAAAAAA 438
DB 361 CCGGAACTTCTGTTCAATCCAGCGGTCTTACACAGAAAAAGCTGTGATGAAAAAA 420
QY 439 AGAAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTCTG 498
DB 421 AGAAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTCTG 480
QY 499 TATTCCTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTCTG 525
DB 481 TATTCCTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTCTG 507

RESULT 3
AAH98515/c
ID AAH98515 standard; cDNA: 538 BP.
XX
AC AAH98515;
XX
DT 12-OCT-2001 (first entry)
DE Human EST-derived coding sequence SEQ ID NO: 372.
XX
KW Human, sheep, pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dzmanac RA, Zhang J, Werhman T;
XX
XX WPI; 2001-476164/51.
DR P-PSDB; AAM23856.
XX
```

```
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 451; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;
XX
Query Match 93.3%; Score 498.2; DB 22; Length 538;
Best Local Similarity 99.4%; Pred. No. 1.5e-99;
Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 15 GTGAAGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTGCTCCGCCGGTGGCGGTGCT 74
DB 503 GGGAAAGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTGCTCCGCCGGTGGCGGTGCT 444
QY 75 ATGCTTTCGAGAACTTACTCAGGCAAGCACTGAGAAAGTTGAGGAAAGTGTGCTG 134
DB 443 ATGCTTTCGAGAACTTACTCAGGCAAGCACTGAGAAAGTTGAGGAAAGTGTGCTG 384
QY 135 CTGGGCTCTGCAAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 194
DB 383 CTGGGCTCTGCAAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 324
QY 195 TCAGTGGAAAGGCGAGTGAAGATGCTGGGCTGATATTTATCACTCACTGTAACAA 254
DB 323 TCAGTGGAAAGGCGAGTGAAGATGCTGGGCTGATATTTATCACTCACTGTAACAA 264
QY 255 CAGTATTCATGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 314
DB 263 CAGTATTCATGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 204
QY 315 TTGGTGGAGGGGTGTTGCACTTGGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 374
DB 203 TTGGTGGAGGGGTGTTGCACTTGGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 144
QY 375 TTACCGGGAAGCTTCTGTTCAATCCAGCGGTCTTACACAGAAAAAGCTGTGATGAAA 434
DB 143 TTACCGGGAAGCTTCTGTTCAATCCAGCGGTCTTACACAGAAAAAGCTGTGATGAAA 84
QY 435 AAAAAGAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 494
DB 83 AAAAAGAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 24
QY 495 TCTGATTTCTTCAAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTCTG 517
DB 23 TCTGATTTCTTCAAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTCTG 1

RESULT 4
AAH98548/c
ID AAH98548 standard; cDNA: 538 BP.
XX
AC AAH98548;
XX
DT 12-OCT-2001 (first entry)
DE Human EST-derived coding sequence SEQ ID NO: 405.
XX
KW Human, sheep, pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
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XX WO200154477-A2.
PN 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US02687.
PD 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX (HXXSE-) HXXSEQ INC.
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dirmannac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
DR P-PSDB; AAM23889.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 467; 1275BP; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;
Query Match 93.3%; Score 498.2; DB 22; Length 538;
Best Local Similarity 99.4%; Pred. No. 1.5e-99;
Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 15 GTGAAGCCGAGCTGGGCGAGAAAGTGGGAGGCGGCTCCGCGCGTGGCGGCTTCT 74
DB 503 GGGAGGCGGAGCTGGGCGAGAAAGTGGGAGGCGGCTCCGCGCGTGGCGGCTTCT 444
QY 75 ATCCGTTGCGAGAACTTACTCAGGAGCGAGCTGAGAAAGTGGGAGGCGGCTGCTG 134
DB 443 ATCCGTTGCGAGAACTTACTCAGGAGCGAGCTGAGAAAGTGGGAGGCGGCTGCTG 384
QY 135 CTGGGCTGCGAGAGCGGATGATTAACGTCAGCCGAGAAATTAACATGCGCCCTTCTGCT 194
DB 383 CTGGGCTGCGAGAGCGGATGATTAACGTCAGCCGAGAAATTAACATGCGCCCTTCTGCT 324
QY 195 TCAGTGTGAAGGCGGAGGATGCTGGGCGGCTGAGATTAATCACTCACTGGTAAACA 254
DB 323 TCAGTGTGAAGGCGGAGGATGCTGGGCGGCTGAGATTAATCACTCACTGGTAAACA 264
QY 255 CAGTATTCATGCTCATCTGCTGTTGGGAGCTGATACAGAAACCAACATTTGACAG 314
DB 263 CAGTATTCATGCTCATCTGCTGTTGGGAGCTGATACAGAAACCAACATTTGACAG 204
QY 315 TTGGTGAAGGGGTGTTTGCACCTTGTGACAGAGTATGCTGTCGCGAGCGGGCCCTTA 374
DB 203 TTGGTGAAGGGGTGTTTGCACCTTGTGACAGAGTATGCTGTCGCGAGCGGGCCCTTA 144
QY 375 TTTCACCGGAAGCTTGTGTTCAATCCAGCGGCTCTTACCAAGAAAGCTGTGATGAAA 434
DB 143 TTTCACCGGAAGCTTGTGTTCAATCCAGCGGCTCTTACCAAGAAAGCTGTGATGAAA 84
QY 435 AAAAGAGAGTTTGTGATTTATATATTTATTTTATTTAGTTGATAGTAAATTAACATATT 494
DB 83 AAAAGAGAGTTTGTGATTTATATTTATTTTATTTAGTTGATAGTAAATTAACATATT 24
QY 495 TCTGTATTCTTCCAAAAA 517

DB 23 TCTGTATTCTTAAAAA 1
RESULT 5
ID AAH34835
XX AAH34835 standard; cDNA; 558 BP.
AC AAH34835;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG75430.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 3428; 9803BP; English.
XX
CC AAH32943 to AAH37195 and AAG75430 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated P,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAG77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;
Query Match 93.1%; Score 497.2; DB 22; Length 558;
Best Local Similarity 98.4%; Pred. No. 2.5e-99;
Matches 499; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 16 TGAAGCCGAGCTGGGCGAGAGTGAAGGAGGCGGCTCCGCGCGTGGCGGCTTCTA 75
DB 11 TGAAGGCGAGCTGGGCGAGAGTGAAGGAGGCGGCTCCGCGCGTGGCGGCTTCTA 70
QY 76 TCGGTTGCGAGAACTTACTCAGGAGCGAGCTGAGAAAGTGAAGGAAAGTCTGCTGC 135
DB 71 TCGGTTGCGAGAACTTACTCAGGAGCGAGCTGAGAAAGTGAAGGAAAGTCTGCTGC 130

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Qy 136 TGGGCTTCGACAGCCGATGATTAAGTGCAGCCGAAATTAACATGCCCCCTTCTGCTT 195
Dy 131 TGGGCTTCGACAGCCGATGATTAAGTGCAGCCGAAATTAACATGCCCCCTTCTGCTT 190
Qy 196 CAGGTGTAAGGCGACCGTAAGATGCTGCGGCTGATTTTCAACTCATTGTAACAC 255
Dy 191 CAGGTGTAAGGCGACCGTAAGATGCTGCGGCTGATTTTCAACTCATTGTAACAC 250
Qy 256 AGTATTCATGCTCATGCTGATCTGTTGGCACTGATACCAAAACCAACATTGACAGT 315
Dy 251 AGTATTCATGCTCATGCTGATCTGTTGGCACTGATACCAAAACCAACATTGACAGT 310
Qy 316 TGGTGAAGGGGTGTTTGGCACTTGTGACAGAGTAAGTGTCTTGGCCGAGCGGCGCTTAT 375
Dy 311 TGGTGAAGGGGTGTTTGGCACTTGTGACAGAGTAAGTGTCTTGGCCGAGCGGCGCTTAT 370
Qy 376 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTTGTGATGAATA 435
Dy 371 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTTGTGATGAATA 430
Qy 436 AAAAGAAGTTTGTATTTATTTATTTACTTTTATGTTGATTAAGTATTAACATATTT 495
Dy 431 AAAAGAAGTTTGTATTTATTTATTTACTTTTATGTTGATTAAGTATTAACATATTT 490
Qy 496 CTGTATTTCTTCCAAAAAATTTTTTTTTT 522
Dy 491 CTGTATTTCTTCCAAAAAATTTTTTTTTT 517
```

RESULT 6
ID AAA87730 standard; cDNA; 515 BP.

AC AAA87730;

DT 28-NOV-2000 (first entry)

DE Human secreted protein encoding cDNA SEQ ID #29.

XX Human; secreted protein; forensic procedure; gene therapy;
XX chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
XX cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
XX brain disorder; skeletal muscle disorder; obesity;
XX mitochondrial cytopathy; diabetes; atherosclerosis; Alzheimer's disease;
XX neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
XX septic shock; impotence; ss.

OS Homo sapiens.

PN WO200037491-A2.

PD 29-JUN-2000.

PF 20-DEC-1999; 99WO-1B02058.

PR 22-DEC-1998; 98US-0113686.

PR 25-JUN-1999; 99US-0141032.

XX (GIST) GENSET.

PI Bougueleret L, Dumas J, Duclert A;

DR WPI; 2000-442637/38.

DR P-PSDB; AAB25768.

XX Polynucleotides and polypeptides encoding proteins with signal
XX peptides, useful in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures -

PS Claim 1; Page 169-170; 306pp; English.

XX This sequence represents human cDNA encoding a secreted protein. The

CC invention relates to sequences AAA87725-A87774 which encode human
CC secreted proteins AAB25763-B25812. The proteins include signal peptides.
CC included in the invention are a host cell containing one of the cDNA
CC sequences, and a purified antibody capable of binding to one of the
CC secreted proteins. Also contained in the invention are methods for
CC storing the sequence data on a computer system, and a method for
CC identifying features of the cDNA sequences using a computer programme.
CC The cDNAs are useful for expressing secreted proteins or fragments to
CC obtain antibodies capable of specifically binding to the secreted
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
CC therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence.

CC Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

XX Query Match 92.4%; Score 493.4; DB 21; Length 515;

XX Best Local Similarity 99.4%; Pred. No. 1.7e-98; Mismatches 2; Indels 1; Gaps 1;

XX Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 15 GTGAAGCCGAGCTGGGCGAGAGTAGGGGAGGGGCTCCGCGGCTGGCGGTTGCT 74
Dy 8 GGGAGCCGAGCTGGGCGAGAGTAGGGGAGGGGCTCCG CGGGTGGCGTTGCT 66

Qy 75 ATCGCTTCGCAAGACCTACTCAGGACCCAGCTGAGAAAGTTGAGGAAAGTCTCTG 134

Dy 67 ATCGCTTCGCAAGACCTACTCAGGACCCAGCTGAGAAAGTTGAGGAAAGTCTCTG 126

Qy 135 CTGGGCTCGAGAGCGAGTGAATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTGCT 194

Dy 127 CTGGGCTCGAGAGCGAGTGAATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTGCT 186

Qy 195 TCAAGTGAAGGCGACGTGAAGATGCTGCGGCTGATATTTATCACTGATGAACAA 254

Dy 187 TCAAGTGAAGGCGACGTGAAGATGCTGCGGCTGATATTTATCACTGATGAACAA 246

Qy 255 CAGTATTCATGCTCATGATGTTCTGTGGCACTGATACCAAAACCAACATTGACAG 314

Dy 247 CAGTATTCATGCTCATGATGTTCTGTGGCACTGATACCAAAACCAACATTGACAG 306

Qy 315 TTGGTGAAGGGGTGTTGCACTTGTGACAGAGTATGCTTGGCGAGGGGCGCTTA 374

Dy 307 TTGGTGAAGGGGTGTTGCACTTGTGACAGAGTATGCTTGGCGAGGGGCGCTTA 366

Qy 375 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTGTGATGAATA 434

Dy 367 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTGTGATGAATA 426

Qy 435 AAAAAGAAGTTTGTAAATTTTATTTACTTTTATGTTGATTAAGTATTAACATATT 494

Dy 427 AAAAAGAAGTTTGTAAATTTTATTTACTTTTATGTTGATTAAGTATTAACATATT 486

Qy 495 TCTGTATTTCTTCCAAAAAATTTTTTTTTT 522

Dy 487 TCTGTATTTCTTCCAAAAAATTTTTTTTTT 514

RESULT 7

AAFe4012

AC AAF64012;

DT 05-APR-2001 (first entry)

DE cDNA encoding human secreted protein #13.

XX Secreted protein; prevention; treatment; diagnosis; disease;

XX infection; de.
XX Homo sapiens.
XX MO200100806-A2.
XX 04-JAN-2001.
XX 21-JUN-2000; 2000WO-IB00951.
XX 25-JUN-1999; 99US-0141032.
XX 21-DEC-1999; 99US-0469039.
XX (GEST) GENSET.
XX Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX WPI; 2001-071487/08.
XX
XX 49 Secreted proteins and the nucleic acids encoding them, useful in
XX gene therapy and for detecting similar sequences in samples -
XX
XX Claim 1; Page 225; 307pp; English.
XX
XX The present invention relates to 49 Secreted proteins and the cDNAs
XX encoding them. The protein and nucleic acids may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate protein expression.
XX
XX Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;
SQ
Query Match 92.4%; Score 493.4; DB 22; Length 515;
Best Local Similarity 99.4%; Pred. No. 1.7e-98;
Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 15 GTGAAGCCGAGCTGGCGGAGAGTGGGAGGCGGCTCCCGCGGCTGCGGCTGCT 74
DB 8 GGGAGGCGGAGCTGGCGGAGAGTGGGAGGCGGCTCCG-CGGGCTGCGGCTGCT 66
QY 75 ATGCGCTTCGAGAACTACTCAGCAGCAGCAGCTGAGAGAGTTGAGGGAAAGTCTCTG 134
DB 67 ATGCGCTTCGAGAACTACTCAGCAGCAGCAGCTGAGAGAGTTGAGGGAAAGTCTCTG 126
QY 135 CTGGGCTGCGAGAGCGATGATTAACGTGACCGGAAATTAACATCGCCCTTCTGCT 194
DB 127 CTGGGCTGCGAGAGCGATGATTAACGTGACCGGAAATTAACATCGCCCTTCTGCT 186
QY 195 TCAGTGGAAGAGCGACGTGAAGTGTCTGGCTGATATTATTAATCTACTGTGTAACA 254
DB 187 TCAGTGGAAGAGCGACGTGAAGTGTCTGGCTGATATTATTAATCTACTGTGTAACA 246
QY 255 CAGTATTCATGCTCATGCTATCTGTGTCAGTATGACAGAAACACAAACATTGACAG 314
DB 247 CAGTATTCATGCTCATGCTATCTGTGTCAGTATGACAGAAACACAAACATTGACAG 306
QY 315 TTGGTGAAGGGGTGTTGCACTTGTCAGACAGATATCTGCTCCGAGCGGGCCCTTA 374
DB 307 TTGGTGAAGGGGTGTTGCACTTGTCAGACAGATATCTGCTCCGAGCGGGCCCTTA 366
QY 375 TTTAACCGGAAGCTTCTGTTCAATCCAGCGGCTCTTAACAGAAAGCCGTGTCATAA 434
DB 367 TTTAACCGGAAGCTTCTGTTCAATCCAGCGGCTCTTAACAGAAAGCCGTGTCATAA 426
QY 435 AAAAAGAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 494
DB 427 AAAAAGAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 486
QY 495 TCTGTATTTCTCCAAAAAATTTAAAAA 522
DB 487 TCTGTATTTCTCCAAAAAATTTAAAAA 514

AAV59598
ID AAV59598 standard; DNA; 504 BP.
XX AC AAV59598;
XX DT 06-JAN-1999 (first entry)
XX DE Human secreted protein gene 88 clone HAAVAV32.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal; de;
XX immune system; ascites; lymphocytic disease; brain; hepatic lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; retinosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX Homo sapiens.
XX PN MO9839448-A2.
XX PD 11-SEP-1998.
XX
XX 06-MAR-1998; 98WO-US04493.
XX PF 02-OCT-1997; 97US-0061060.
XX PR 07-MAR-1997; 97US-0038621.
XX PR 07-MAR-1997; 97US-0040161.
XX PR 07-MAR-1997; 97US-0040162.
XX PR 07-MAR-1997; 97US-0040163.
XX PR 07-MAR-1997; 97US-0040333.
XX PR 07-MAR-1997; 97US-0040334.
XX PR 07-MAR-1997; 97US-0040336.
XX PR 11-MAR-1997; 97US-0040626.
XX PR 11-APR-1997; 97US-0043311.
XX PR 11-APR-1997; 97US-0043312.
XX PR 11-APR-1997; 97US-0043313.
XX PR 11-APR-1997; 97US-0043314.
XX PR 11-APR-1997; 97US-0043568.
XX PR 11-APR-1997; 97US-0043569.
XX PR 11-APR-1997; 97US-0043576.
XX PR 11-APR-1997; 97US-0043578.
XX PR 11-APR-1997; 97US-0043580.
XX PR 11-APR-1997; 97US-0043669.
XX PR 11-APR-1997; 97US-0043670.
XX PR 11-APR-1997; 97US-0043671.
XX PR 11-APR-1997; 97US-0043672.
XX PR 11-APR-1997; 97US-0043674.
XX PR 23-MAY-1997; 97US-0047492.
XX PR 23-MAY-1997; 97US-0047500.
XX PR 23-MAY-1997; 97US-0047501.
XX PR 23-MAY-1997; 97US-0047502.
XX PR 23-MAY-1997; 97US-0047503.
XX PR 23-MAY-1997; 97US-0047581.
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XX PR 23-MAY-1997; 97US-0047585.
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XX PR 23-MAY-1997; 97US-0047587.
XX PR 23-MAY-1997; 97US-0047588.
XX PR 23-MAY-1997; 97US-0047589.
XX PR 23-MAY-1997; 97US-0047590.
XX PR 23-MAY-1997; 97US-0047592.
XX PR 23-MAY-1997; 97US-0047593.
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XX PR 23-MAY-1997; 97US-0047595.
XX PR 23-MAY-1997; 97US-0047596.
XX PR 23-MAY-1997; 97US-0047597.
XX PR 23-MAY-1997; 97US-0047598.
XX PR 23-MAY-1997; 97US-0047599.
XX PR 23-MAY-1997; 97US-0047600.

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	PR	23-MAY-1997;	97US-0047612.
	PR	23-MAY-1997;	97US-0047613.
	PR	23-MAY-1997;	97US-0047614.
	PR	23-MAY-1997;	97US-0047615.
	PR	23-MAY-1997;	97US-0047617.
	PR	23-MAY-1997;	97US-0047618.
	PR	23-MAY-1997;	97US-0047632.
	PR	23-MAY-1997;	97US-0047633.
	PR	06-JUN-1997;	97US-0048964.
	PR	06-JUN-1997;	97US-0048974.
	PR	13-JUN-1997;	97US-0049610.
	PR	08-JUL-1997;	97US-0051926.
	PR	16-JUL-1997;	97US-0052874.
	PR	18-AUG-1997;	97US-0055724.
	PR	22-AUG-1997;	97US-0056630.
	PR	22-AUG-1997;	97US-0056631.
	PR	22-AUG-1997;	97US-0056632.
	PR	22-AUG-1997;	97US-0056636.
	PR	22-AUG-1997;	97US-0056637.
	PR	22-AUG-1997;	97US-0056662.
	PR	22-AUG-1997;	97US-0056664.
	PR	22-AUG-1997;	97US-0056685.
	PR	22-AUG-1997;	97US-0056842.
	PR	22-AUG-1997;	97US-0056864.
	PR	22-AUG-1997;	97US-0056872.
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	PR	22-AUG-1997;	97US-0056875.
	PR	22-AUG-1997;	97US-0056876.
	PR	22-AUG-1997;	97US-0056877.
	PR	22-AUG-1997;	97US-0056878.
	PR	22-AUG-1997;	97US-0056879.
	PR	22-AUG-1997;	97US-0056880.
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	PR	22-AUG-1997;	97US-0056882.
	PR	22-AUG-1997;	97US-0056884.
	PR	22-AUG-1997;	97US-0056886.
	PR	22-AUG-1997;	97US-0056887.
	PR	22-AUG-1997;	97US-0056888.
	PR	22-AUG-1997;	97US-0056889.
	PR	22-AUG-1997;	97US-0056892.
	PR	22-AUG-1997;	97US-0056893.
	PR	22-AUG-1997;	97US-0056894.
	PR	22-AUG-1997;	97US-0056897.
	PR	22-AUG-1997;	97US-0056908.
	PR	22-AUG-1997;	97US-0056909.
	PR	22-AUG-1997;	97US-0056910.
	PR	22-AUG-1997;	97US-0056911.
	PR	05-SEP-1997;	97US-0057650.
	PR	05-SEP-1997;	97US-0057669.
	PR	05-SEP-1997;	97US-0057761.
	PR	12-SEP-1997;	97US-0058785.
XX	(HUMA-) HUMAN GENOME SCI INC.		
XA			
XB	Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,		
XI	Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;		
P1	Kyag H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,		
R1	Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;		
XX	WPI; 1998-506364/43.		
DR	P-PDB; AAW74818.		
XX			
PT	New isolated human genes and the secreted polypeptide(s) they encode		
PT	- useful for diagnosis and treatment of e.g. cancers, neurological		
PT	disorders, immune diseases, inflammation or blood disorders		
XX			
PS	Claim 1; Page 320; 721pp; English.		
CC	This sequence represents a nucleic acid molecule designated Gene 88 from		
CC	the human CDNA clone HUANV32 (deposited as clone ATCC 97901 and ATCC		
CC	2050477) which encodes a secreted human protein. The gene can be used to		
CC	generate fusion proteins by linking to the gene to a human		

CC	immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
CC	the fused protein as compared to the human protein only.
CC	The invention relates to 186 novel genes and their fragments (nucleic
CC	acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
CC	which are useful for preventing, treating or ameliorating medical
CC	conditions e.g. by protein or gene therapy. Also, pathological conditions
CC	can be diagnosed by determining the amount of the new polypeptides in a
CC	sample or by determining the presence of mutations in the new
CC	polynucleotides. Specific uses are described for each of the 186
CC	polynucleotides, based on which tissues they are most highly expressed in
CC	(see AAV59511 for described uses).
XX	
XX	
SQ	Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;
Query Match	91.1%; Score 486.6; DB 19; Length 504;
Best Local Similarity	99.0%; Pred. No. 5.1e-97;
Matches 500;	Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY	21 CCGAGCTGGCGGAGAAAGTAGGGGAGGGGGGTCTCCGCGGGTGGCGGTTCATAGCT 80
DB	1 CCGAGCTGGCGGAGAAAGTAGGGGAGGGGCG -ACGACCCGCGGGGCGGTTCATAGCT 59
QY	81 TCGAGAAACCTACTCCAGGCACGACGTGAGAAAGTTGAGGGAAGATCTGCTGGGT 140
DB	60 TCGCAAACTTACTCAGGACCGACTTGAGAGAGTTGAGGAAAGTCTGCTGGGT 119
QY	141 CTGCAGACGCGATGATATACGTGACGCGGAAATATAAACATCGCCCTTCGCTTCACTG 200
DB	120 CTGCAGACGCGATGATATACGTGACGCGGAAATATAAACATCGCCCTTCGCTTCACTG 179
QY	201 TGAAGGCGCAGTGAAGATGCTGCGGGCTGATATTTATCACTCACTGTTAAACAACAGTAT 260
DB	180 TGAAGGCGCAGTGAAGATGCTGCGGGCTGATATTTATCACTCACTGTTAAACAACAGTAT 239
QY	261 TCATGCTCATGTATCTGTGTGTGCACTGATACAGAGAAACCAACAACATGTACAGTTGGTG 320
DB	240 TCATGCTCATGTATCTGTGTGTGCACTGATACAGAGAAACCAACAACATGTACAGTTGGTG 299
QY	321 GAGGGGTTTGTGCACTTGTGACACAGATGCTGCTTTCGCGAGGGGCGCTTATTTTACC 380
DB	300 GAGGGGTTTGTGCACTTGTGACACAGATGCTGCTTTCGCGAGGGGCGCTTATTTTACC 359
QY	361 GGAAGCTTCTGTCAATCCACGCGGTCTTACCAAGAAAAGCCTGTGCATGAAAAAAG 440
DB	360 GGAAGCTTCTGTCAATCCACGCGGTCTTACCAAGAAAAGCCTGTGCATGAAAAAAG 419
QY	441 AAGTTTGTATTTTATATTAATCTTTTGTATGATACATATATTAACATATTTCTGTGA 500
DB	420 AAGTTTGTATTTTATATTAATCTTTTGTATGATACATATATTAACATATTTCTGTGA 479
QY	501 TTCTTCCAAAAAATTTTTTTTTTAAAA 525
DB	480 TTCTTCCAAAAAATTTTTTTTTTAAAA 504
RESULT 9	
AB573585	
ID	AB573585 standard; cDNA; 504 BP.
XX	
XX	AB573585;
DT	
XX	
DE	15-JAN-2003 (first entry)
XX	
XX	Human cDNA #1 for novel secreted protein gene 88.
KM	Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
KM	rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KM	liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KM	cerebrovascular disorder; cerebral ischemia; angiogenesis; sunburn;
KM	nervous system disorders; Alzheimer's disease; infection;
KM	ocular disorder; corneal infection; wound healing; tissue regeneration;
KM	epithelial cell proliferation; organ transplantation; food additive;
KM	preservative; nutritional.

PR 11-APR-1997; 97US-043576P.
 PR 11-APR-1997; 97US-043578P.
 PR 11-APR-1997; 97US-043580P.
 PR 11-APR-1997; 97US-043669P.
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 PR 23-MAY-1997; 97US-047492P.
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 PR 23-MAY-1997; 97US-047502P.
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 PR 23-MAY-1997; 97US-047612P.
 PR 23-MAY-1997; 97US-047613P.
 PR 23-MAY-1997; 97US-047614P.
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 PR 23-MAY-1997; 97US-047633P.
 PR 06-JUN-1997; 97US-048964P.
 PR 06-JUN-1997; 97US-048974P.
 PR 13-JUN-1997; 97US-049610P.
 PR 08-JUL-1997; 97US-051926P.
 PR 16-JUL-1997; 97US-052874P.
 PR 18-AUG-1997; 97US-055724P.
 PR 22-AUG-1997; 97US-056630P.
 PR 22-AUG-1997; 97US-056631P.
 PR 22-AUG-1997; 97US-056632P.
 PR 22-AUG-1997; 97US-056633P.
 PR 22-AUG-1997; 97US-056637P.
 PR 22-AUG-1997; 97US-056662P.
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 PR 22-AUG-1997; 97US-056845P.
 PR 22-AUG-1997; 97US-056862P.
 PR 22-AUG-1997; 97US-056864P.
 PR 22-AUG-1997; 97US-056872P.
 PR 22-AUG-1997; 97US-056874P.
 PR 22-AUG-1997; 97US-056875P.
 PR 22-AUG-1997; 97US-056876P.
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 PR 22-AUG-1997; 97US-056892P.

PR 22-AUG-1997; 97US-056893P.
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 PR 22-AUG-1997; 97US-056903P.
 PR 22-AUG-1997; 97US-056909P.
 PR 22-AUG-1997; 97US-056909P.
 PR 22-AUG-1997; 97US-056910P.
 PR 22-AUG-1997; 97US-056911P.
 PR 22-AUG-1997; 97US-057611P.
 PR 05-SEP-1997; 97US-057650P.
 PR 05-SEP-1997; 97US-057669P.
 PR 12-SEP-1997; 97US-058785P.
 PR 02-OCT-1997; 97US-061060P.
 PR 06-MAR-1998; 98WO-US04493.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
 PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX WPI: 2002-634796/68.
 DR P-PSDB; ABG95421.
 XX
 PT New isolated human secreted protein for diagnosing, preventing,
 PT treating or ameliorating medical conditions and used as a food additive
 PT or preservative
 XX
 XX Example 1; SEQ ID No 252; 129pp; English.
 XX
 CC The invention relates to an isolated protein that is one of 186 human
 CC secreted proteins, given in the specification, encoded by one of
 CC 309 cDNA sequences also given in the specification. The protein is used
 CC in a pharmaceutical composition used to prevent, treat or ameliorate a
 CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
 CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. The present sequence represents a cDNA derived from a
 CC gene encoding one of the novel human secreted proteins of the invention.
 CC Note: This sequence did not form part of the printed specification,
 CC but was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=642052651.
 CC
 XX
 SQ Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;
 QY
 QY Query Match 89.6%; Score 478.6; DB 24; Length 506;
 QY Best Local Similarity 97.4%; Pred. No. 2.8e-95;
 QY Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 Db 37 GTAGGAGGAGCGGCTGCTCCGCGCGGCTGCTATCGCTTCAGCAACTACTCA 96
 Db 2 GCAGGATTGGCCAGAGCCSCCGCGGTGGCTGTATCGCTTCAGCAACTACTCA 61
 QY 97 GGCAGCAGCTGAGAGAGATTGAGGGAAGTCTGCTGCTGCTGCTGCAACGGATGCA 156
 Db 62 GGCAGCAGCTGAGAGAGATTGAGGGAAGTCTGCTGCTGCTGCTGCAACGGATGCA 121
 QY 157 TTAAGTCAGCCGCAAAATTAACAATGCGCCCTTCTGTTAGTGTGAAGCAACGGTAA 216
 Db 122 TTAAGTCAGCCGCAAAATTAACAATGCGCCCTTCTGTTAGTGTGAAGCAACGGTAA 181
 QY 217 GATGCTCGGCTGATATTATCAACTCTGTAAACAAGTATTCATGCTCATCGTATC 276

```

Db      182 GATCTGGCGCTGATATTAATCACTCACTGTAACAAACAGTATTCATGTCATCGTATC 241
Qy      277 TGTGTGGCACTGATATACAGAAACCAACAACTGACAGTGTGGAGGGGTTTGCACT 336
Db      242 TGTGTGGCACTGATATCAAGAAACCAACAACTGACAGTGTGGAGGGGTTTGCACT 301
Qy      337 TGTGACAGCAGTATGCTGTCTTGGCGAGGGGCCCTTATTTACGGAAGCTTCTGTCAA 396
Db      302 TGTGACAGCAGTATGCTGTCTTGGCGAGGGGCCCTTATTTACGGAAGCTTCTGTCAA 361
Qy      397 TCCAGCGGCTCTTACCAAGAAAAGCCTGTGATGAAAAAAGAGTTTGTATTTTA 456
Db      362 TCCAGCGGCTCTTACCAAGAAAAGCCTGTGATGAAAAAAGAGTTTGTATTTTA 421
Qy      457 TATTAATCTTTAGTTAGTATGATTAATTAACATTTCTGTATCTTCCAAAAAAA 516
Db      422 TATTAATCTTTAGTTAGTATGATTAATTAACATTTCTGTATCTTCCAAAAAAA 481
Qy      517 AAAAAAAAAAAAAAAAAA 533
Db      482 AAAAAAAAAAAAAAAAAA 498

```

RESULT 12
AAK97826
ID AAK97826 standard; cDNA; 500 BP.

AAK97826;
23-SEP-1999 (first entry)

Human secreted protein encoding cDNA #14.

Secreted protein; human; cytosolic; chromoblastic; osteopathic; forensic;
diagnostic; gene therapy; chromosome mapping; secretion vector; ss.

Homo sapiens.

WO9925825-A2.

27-MAY-1999.

13-NOV-1998; 98WO-1B01862.

04-SEP-1998; 98US-0099272.

13-NOV-1997; 97US-0066677.

17-DEC-1997; 97US-0069957.

09-FEB-1998; 98US-0074121.

13-APR-1998; 98US-0081563.

10-AUG-1998; 98US-0096116.

(GENSET) GENSET.

Bouguetieret L, Duclet A, Dumas Milne Edwards J;

WPI, 1999-347472/29.

P-PSDB; AAY36142.

Extended cDNAs encoding secreted proteins

Example 26; Page 173-174; 307bp; English.

AAK97813-X97906 represent extended cDNA's which encode novel human
secreted proteins (see AAY36129-Y36222) and which have cytosolic,
chromoblastic and osteopathic activity. The extended cDNAs can be used to
express secreted proteins or parts of them or to obtain antibodies
capable of binding to the secreted proteins. They may also be used in
diagnostic, forensic, gene therapy and chromosome mapping procedures.
Uses also include design of expression vectors and secretion vectors.

Query Match 87.4%; Score 466.8; DB 20; Length 500;
Best Local Similarity 97.8%; Pred. No. 1.1e-92;
Matches 488; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

```

Qy      23 GAGCTGGCGCAAGATGAGGAGGAGGCGGCTCCGCGCGTGGCCG-TTGCTATGGCTT 81
Db      2 GAGCTGNNCNSAAGTGGAGGAGGCGGCTCCGCGCGTGGCCGCGGDBTGTATGCTT 61
Qy      82 CGCAGAACTTACTCAGGCAAGCAGTGAAGAGTTGAGGAAAGTCTGCTGGTGC 141
Db      62 CGCAGAACTTACTCAGGCAAGCAGTGAAGAGTTGAGGAAAGTCTGCTGGTGC 121
Qy      142 TGACAGCGCATGATACCTGACGCCGAAATTAACATCGCCCTTCTGCTTCA 201
Db      122 TGACAGCGCATGATACCTGACGCCGAAATTAACATCGCCCTTCTGCTTCA 181
Qy      202 GAAAGCGCAGTGA-AGATCTCGCGCTGGATTTATCACTGATGATCAACAGTAT 260
Db      182 GAAAGCGCAGTGAAGATGCTCGCGCTGGATTTATCACTGATGATCAACAGTAT 241
Qy      261 TCATGCTCATGCTATCTGTGTGGCACTGATACCAAGAAACCAACATTTGACAGTTG 320
Db      242 TCATGCTCATGCTATCTGTGTGGCACTGATACCAAGAAACCAACATTTGACAGTTG 301
Qy      321 GAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTCTTGGCAGCGGGCCCTTATTTAC 380
Db      302 GAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTCTTGGCAGCGGGCCCTTATTTAC 361
Qy      381 GGAAGCTTCTGTTCAATCCAGCGGCTCTTACCAAGAAAGCCTGTGCAATGAAAAAAG 440
Db      362 GGAAGCTTCTGTTCAATCCAGCGGCTCTTACCAAGAAAGCCTGTGCAATGAAAAAAG 421
Qy      441 AAGTTTGTATTTTATTTATTTAGTTTGTGATGATTAACATATTTCTGTA 500
Db      422 AAGTTTGTATTTTATTTATTTAGTTTGTGATGATTAACATATTTCTGTA 481
Qy      501 TTCTTCCAAAAA 519
Db      482 TTCTTCCAAAAA 500

```

RESULT 13
AAAI5929
ID AAI5929 standard; cDNA; 467 BP.

AAAI5929;

12-JUN-2000 (first entry)

Human protein clone HP10357 full length coding sequence.

Human protein; hydrophobic domain; nutritional source; haematopoiesis;
cytokine production; cell proliferation; cell differentiation;
immune deficiency; infectious disease; autoimmune disorder; asthma;
multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
nervous system disorder; Alzheimer's disease; Parkinson's disease;
Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
systemic cytokine damage; tissue differentiation; contraceptive; stroke;
coagulation disorder; myocardial infarction; inflammatory condition;
septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
nephritis; therapy; ss.

Homo sapiens.

WO200005367-A2.

03-FEB-2000.

22-JUL-1999; 99WO-JP03929.

24-JUL-1998; 98JP-0208820.

07-AUG-1998; 98JP-0224105.

PR 25-AUG-1998; 98JP-0238116.
PR 09-SEP-1998; 98JP-0254736.
PR 29-SEP-1998; 98JP-0275505.
XX
XX (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
XX Kato S, Kimura T;
XX WPI; 2000-182694/16.
DR P-PSDB; AAY94861.
XX
XX Novel human proteins having hydrophobic domains useful for treating
PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
XX
PS Claim 4; Page 228; 351pp; English.
XX
XX This sequence encodes a human protein of the invention, which has
CC hydrophobic domains. The DNA sequences can be used as a probe or as a
CC genetic marker. The protein can also be used as a marker, and to identify
CC potential genetic disorders. The DNA and protein can also be used as
CC nutritional sources or supplements. The protein exhibits cytokine, cell
CC proliferation, cell differentiation activities and induces production of
CC other cytokines in certain cell populations. The protein also exhibits
CC immune stimulating or immune suppressing activity. It can be used in the
CC treatment of various immune deficiencies and disorders, and to treat
CC infectious diseases caused by viral, bacterial, fungal or other
CC infections. The protein is also used for treating autoimmune disorders
CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
CC arthritis. It is also useful in the treatment of allergic reactions and
CC conditions such as asthma, and in immune suppression after organ
CC transplantation. The protein is useful in regulation of haematopoiesis
CC and consequently in the treatment of myeloid or lymphoid cell
CC deficiencies. It is also used in compositions for tissue growth or
CC regeneration. The protein is also used in the treatment of osteoporosis
CC or osteoarthritis and in the treatment of periodontal disease and other
CC tooth repair processes. The protein is used in the treatment of nervous
CC system disorders such as Alzheimer's disease, Parkinson's disease, and
CC Huntington's disease. They are useful for protection or regeneration and
CC treatment of lung or liver fibrosis, reperfusion injury in various
CC tissues, and conditions resulting from systemic cytokine damage. They are
CC also used for promoting or inhibiting tissue differentiation. They are
CC also used as contraceptives since they exhibit activin or inhibin related
CC activities and as a fertility inducing therapeutic. They are used for
CC treating various coagulation disorders and in treatment and prevention of
CC conditions resulting from coagulation activities e.g. myocardial
CC infarction or stroke. They also acts as receptors, receptor ligands or
CC inhibitors or agonists of receptor/ligand interactions. They are used to
CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
CC reperfusion injury, arthritis, and nephritis. They can be used to
CC prevent tumours.
XX
XX Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other;
SQ
Query March 87.2%; Score 465.4; DB 21; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.1e-92;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 39 AGGGGAGGCGGCTCTCCGCGCGGTGGGCTTCTATCGCTTGGCAAGAACTTACTGAGG 98
DB 1 AGGGGAGGCGGCTCTCCGCGCGGTGGGCTTCTATCGCTTGGCAAGAACTTACTGAGG 60
QY 99 CAGGCACTAGAGAGAGTGGAGGAAAGTGTCTGCTGGGTCTGCGAGAGCCGATGATA 158
DB 61 CAGCACTAGAGAGAGTGGAGGAAAGTGTCTGCTGGGTCTGCGAGAGCCGATGATA 120
QY 159 ACGTGACGCGAAGATATAAATCATGCGCCCTTCTGCTTCAAGTGTAAAGGCCACGTGAAGA 218
DB 121 ACGTGACGCGAAGATATAAATCATGCGCCCTTCTGCTTCAAGTGTAAAGGCCACGTGAAGA 180
QY 219 TGCTGGCGGTGATATTAATCAACTCTGTTAGAACAGATATTGATCTCATCTG 278

DB 181 TGCTGGCGGTGATATTAATCAACTCTGTTAGAACAGATATTGATCTCATCTG 240
QY 279 TGTTGGCACTGATACAGAAACCAACAATTTGACAGTTGGTGGAGGGTGTTCACCTTG 338
DB 241 TGTTGGCACTGATACAGAAACCAACAATTTGACAGTTGGTGGAGGGTGTTCACCTTG 300
QY 339 TGAACAGATATGCTGTCTTGGCCGAGGGGCCCTTATTTTACCGGAAGCTTCTGTTCAATC 398
DB 301 TGACAGCAGATATGCTGTCTTGGCCGAGGGGCCCTTATTTTACCGGAAGCTTCTGTTCAATC 360
QY 399 CCAAGCGGTCTTACCAAGAAACCAAGCGTGCATGATAAAGAGTTTGTATTTTATA 458
DB 361 CCAAGCGGTCTTACCAAGAAACCAAGCGTGCATGATAAAGAGTTTGTATTTTATA 420
QY 459 TTACTTTTATTTTATTTGATTAAGTATTAACATATTTTCTGATCTT 505
DB 421 TTACTTTTATTTTATTTGATTAAGTATTAACATATTTTCTGATCTT 467
RESULT 14
ABK36006
ID ABK36006 standard; cDNA; 439 BP.
XX
XX ABK36006;
AC
XX 08-MAY-2002 (first entry)
DT
XX
XX cDNA sequence #397 encoding novel human secreted protein.
DE
XX
XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; allergic condition; neurodegenerative disorder;
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
KW tumour; cancer; hepatotropic; immunosuppressive; antineutlastic; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200177289-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 29-MAR-2001; 2001WO-US10232.
PF
XX
XX 06-APR-2000; 2000US-195605P.
PR
XX
XX (GENY) GENETICS INST INC.
PA
XX
XX Jacobs K, McCreay JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulkota K, Graham JR;
XX
XX WPI; 2002-179322/23.
DR
XX
XX Six hundred and twenty three polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for
PT treating immune deficiencies and disorders such as autoimmune disorders
PT
PS Claim 1; Page 296-297; 393pp; English.
PS
XX
XX The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),
CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.

CC haemophilia), and tumours. The polynucleotide sequences of the
CC invention are also useful in gene therapy. ABK35610-ABK36232 represent
CC the cDNA sequences of the invention that encode for novel human
CC secreted proteins.

XX Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;

Query Match 79.6%; Score 425; DB 24; Length 439;
Best Local Similarity 99.8%; Pred. No. 1,4e-83;
Matches 436; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 72 GCTATCGCTTCGACAGACCTTACTGAGCAGCCAGCTGAGAAAGTTGAGGAAAGTGTG 131
DB 1 GCTATCGCTTCGACAGACCTTACTGAGCAGCCAGCTGAGAAAGTTGAGGAAAGTGTG 60
QY 132 CTGCTGGGTTCGACAGCCGATGATACGTCGACGCCGAAATTAATGATGCCCCCTTCT 191
DB 61 CTGCTGGGTTCGACAGCCGATGATACGTCGACGCCGAAATTAATGATGCCCCCTTCT 120
QY 192 GCTTCAGTGTGAAAGCCAGCTGAAAGATGTCGGCTGGATATTATCACTCACTGTGTA 251
DB 121 GCTTCAGTGTGAAAGCCAGCTGAAAGATGTCGGCTGGATATTATCACTCACTGTGTA 180
QY 252 CAACAGTATTCATGCTCATGCTATCTGTGTGCACTGATACCAAGAAACCAACATTGA 311
DB 181 CAACAGTATTCATGCTCATGCTATCTGTGTGCACTGATACCAAGAAACCAACATTGA 240
QY 312 CAGTGTGTGAGAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTTTCCGACGGGGGCC 371
DB 241 CAGTGTGTGAGAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTTTCCGACGGGGGCC 300
QY 372 TTATTACCGGAAGCTTCGTTCAATCCAGCGGTCCTTACAGAAAGAGCTGTGATG 431
DB 301 TTATTACCGGAAGCTTCGTTCAATCCAGCGGTCCTTACAGAAAGAGCTGTGATG 360
QY 432 AAAAAAAGAAATTGTAATTTTATATTACTTTTATGTTT-GATVACTAAGTATTAAACA 490
DB 361 AAAAAAAGAAATTGTAATTTTATATTACTTTTATGTTTGAATTAAGTATTAAACA 420
QY 491 TATTTCTGATTTCTTCC 507
DB 421 TATTTCTGATTTCTTCC 437

RESULT 15

AAK97873
ID AAK97873 standard; cDNA; 413 BP.

XX AAK97873;

XX 23-SEP-1999 (first entry)

XX Human secreted protein encoding cDNA #61.

XX Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;
KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.

XX Homo sapiens.

XX MO9925825-A2.

XX 27-MAY-1999.

XX 13-NOV-1998; 98WO-IB01862.

XX 04-SEP-1998; 98US-0099273.

XX 13-NOV-1997; 97US-006677.

XX 17-DEC-1997; 97US-006957.

XX 09-FEB-1998; 98US-0074121.

XX 13-APR-1998; 98US-0081563.

XX 10-AUG-1998; 98US-0096116.

PA (GSET) GENSET.

XX Bougueleret L, Duclert A, Dumas Milne Edwards J;
PI WPI: 1999-347472/29.
DR P-PSDB; AAK36189.

XX Extended cDNAs encoding secreted proteins

XX Claim 1; Page 261; 307p; English.

CC AAK97813-X97906 represent extended cDNA's which encode novel human
CC secreted proteins (see AAK36129-Y36222) and which have cytosolic,
CC thrombotic and osteopathic activity. The extended cDNAs can be used to
CC express secreted proteins or parts of them or to obtain antibodies
CC capable of binding to the secreted proteins. They may also be used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC Uses also include design of expression vectors and secretion vectors.

XX Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;

Query Match 77.0%; Score 411.4; DB 20; Length 413;
Best Local Similarity 99.8%; Pred. No. 1.3e-80;
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 107 TGAAGACGTTGAGGAAAGTGTGCTGCTGAGTGTGACAGCCGATGATACGTGACAG 166
DB 1 TGAAGACGTTGAGGAAAGTGTGCTGCTGAGTGTGACAGCCGATGATACGTGACAG 60
QY 167 CCGAAATTAACATGCGCCCTTCTGTGATGATGAAAGCCAGTGAAGATGCTCGCG 226
DB 61 CCGAAATTAACATGCGCCCTTCTGTGATGATGAAAGCCAGTGAAGATGCTCGCG 120
QY 227 CTGGATTTATCACTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 286
DB 121 CTGGATTTATCACTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 287 CTGATACAGAAACCAACATGATGATGATGATGATGATGATGATGATGATGATG 346
DB 181 CTGATACAGAAACCAACATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 347 GATGCTGTCTTCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAAGCT 406
DB 241 GATGCTGTCTTCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAAGCT 300
QY 407 CCTTACAGAAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 466
DB 301 CCTTACAGAAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 467 TAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 519
DB 361 TAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 413

Search completed: January 31, 2004, 02:59:26
Job time : 252 secs

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 02:39:42 ; Search time 2072 Seconds

(without alignments)
6263.798 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534
Sequence: 1 gtcccaatcgtgaag.....aaaaaaaaaaaaa 534

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vtc:*
21: em_gss_vtc:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_pro:*
26: em_gss_rod:*
27: em_gss_phg:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510.2	95.5	548	13	BUS32309
2	507.4	95.0	552	14	CB93661
3	505.8	94.7	524	10	BG705303
4	501.8	94.0	519	13	BX091668

Result No.	Score	Query Match	Length	ID	Description
5	492.4	92.2	528	13	BUS99247
6	492.4	92.2	562	10	BG249994
7	491.8	92.1	510	10	BF399486
8	487	91.2	781	10	BG529072
9	485.4	90.9	487	12	BM472086
10	485.4	90.9	526	13	BUS66499
11	482.4	90.3	534	10	BG031757
12	475	89.0	671	13	BK422104
13	474.4	88.8	1201	13	BK464689
14	469.8	88.0	510	13	BUS65721
15	469.2	87.9	955	13	BUI89908
16	468.2	87.7	529	10	BF691818
17	468	87.6	468	10	BF109912
18	467.6	87.6	930	10	BF203359
19	457.4	85.7	867	13	BUS33237
20	452	84.6	452	9	AI078580
21	446.8	83.7	917	13	BK436125
22	445	83.3	453	9	AI743235
23	438.8	82.2	820	13	BUS66814
24	432.4	81.0	533	9	AA429945
25	430.4	80.6	432	9	AA429945
26	427.8	80.1	466	13	BUS64679
27	427	80.0	427	9	AA455042
28	422	79.0	423	9	AI128804
29	415.2	77.8	443	10	BG613984
30	413.8	77.5	432	9	AV759888
31	412.4	77.2	543	10	BG532587
32	411.8	77.1	1022	13	BUS36995
33	402.6	75.5	815	10	BF215121
34	402.6	75.4	409	9	AI826623
35	400.4	75.0	404	12	BM553628
36	399.4	74.8	402	9	AI989747
37	399	74.7	399	9	AA516431
38	394.4	73.9	396	9	AM183193
39	391	73.2	391	9	AI989739
40	386	72.3	386	9	AA911088
41	384.4	72.0	386	9	AA989129
42	381	71.3	395	9	AI141284
43	374.4	70.1	468	14	W52820
44	363	68.0	522	14	W38899
45	361.6	67.7	389	9	AA305052

ALIGNMENTS

RESULT 1
BUS32309
LOCUS
DEFINITION
AGENCOURT 10202846 NIH_MGC 126 Homo sapiens CDNA clone
IMAGE:5557848 5', mRNA sequence.
ACCESSION
BUS32309
VERSION
BUS32309.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 548)
NIH-MGC http://mgi.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2726 row: 1 column: 16
High quality sequence stop: 516.

Db	331	TTGTGTGAGGGGGTGTTCACCTTGTGACAGACAGATGCTGTCCTTGCCAGCGGGGCCCTTA	390
Qy	375	TTTACCGGAGCTTCTGTTCAATCCGACGGCTCTTACCAAGAAAAGCCTGTGCATGAA	434
Db	391	TTTACCGGAACTTCTGTTCAATCCGACGGCTCTTACCAAGAAAAGCCTGTGCATGAA	450
Qy	435	AAAAAGAGCTTGTGAATTTATATATCTTTTGTGATACATTAAGTATTAACATATT	494
Db	451	AAAAAGAGTTTGTGAATTTATATATCTTTTGTGATACATTAAGTATTAACATATT	510
Qy	495	TCTGTATTCTCCAAAAAAGAAAAA 523	
Db	511	TCTGTATTCTCCAAAAAAGAAAAA 539	
RESULT 3			
LOCUS	BG705303	524 bp	mRNA linear EST 07-MAY-2001
DEFINITION	60268780BP1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4820568 5',		
ACCESSION	BG705303		
VERSION	BG705303.1	GI:13979504	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukacinska, Metaxas, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 524)		
TITLE	NIH-MGC http://mgs.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cga@bbs-rcmail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLM10725 row: 0 column: 01 High quality sequence stop: 521. Location/Qualifiers 1..524 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4820568" /tissue_type="hippocampus" /lab_host="DH10B" /clone_lib="NIH MGC 95" /note="Organ: brain; Vector: pBluescript (modified pBluescript KS+), Site_1: BamHI, Site_2: SalI-XhoI (gtcgagaa); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTV-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."		
FEATURES	source		
BASE COUNT	142 a 113 c 138 g	131 t	
ORIGIN			
Query Match	94.7%;	Score 505.8;	DB 10; Length 524;
Best Local Similarity	99.6%;	Pred. No. 11e-48;	
Matches 507; Conservative	0;	Mismatches 2;	Indels 0; Gaps 0
Qy	15	GTGAAGCCGAGCTGGCGAGAAAGTGGGGAGGGCGGTGCTCCGCGCGGTGGCGGTTGCT	74
Db	4	GGAGAGCCGAGCTGGCGAGAAAGTGGGGAGGGCGGTGCTCCGCGCGGTGGCGGTTGCT	63
Qy	75	ATGCTTGCGACGAACCTACTACGACGACCGACTGAGAAAGATTGAGGGGAATGCTGCTG	134

Db	64	ATGCTTCGCAAGACCTACTCAGGCACCGACTGAAAGACTTGAGGGAAAGTGCTGCTG	123
QY	135	CTGGGCTTCGACAGCGCATGGATACGTGCAGCGGAAATPAAAATCATGCCCTTCTGCT	194
Db	124	CTGGGCTTCGACAGCGCATGGATACGTGCAGCGGAAATPAAAATCATGCCCTTCTGCT	183
QY	195	TCAGTGTGAAAAGGCCAGCTGAAAGATGCTGGCGCTGGAGATATTATATCAATCACTGGTAA	254
Db	184	TCAGTGTGAAAAGGCCAGCTGAAAGATGCTGGCGCTGGAGATATTATCAATCACTGGTAA	243
QY	255	CAGATTTCATGCTCATGCTGATCTGTGTGGACATGCATACAGAAACCAACATTTGACAG	314
Db	244	CAGATTTCATGCTCATGCTGATCTGTGTGGACATGCATACAGAAACCAACATTTGACAG	303
Db	315	TTGGTGGAGGGGTTTGGACCTTGTGACAGCAGATATGCTGTTGGCCAGGGGCCCTT	374
QY	304	TTGGTGGAGGGGTTTGGACCTTGTGACAGCAGATATGCTGTTGGCCAGGGGCCCTT	363
QY	375	TTTACCGGAAAGCTTCTGTTCAATCCGACGGCTCCTTACACAAAAAGCTGTGCATGAA	434
Db	364	TTTACCGGAAAGCTTCTGTTCAATCCGACGGCTCCTTACACAAAAAGCTGTGCATGAA	423
QY	435	AAAAAGAAGTTTGTAATTTATATTAATCTTTAGTTGATACATAAGATTAACATAT	494
Db	424	AAAAAGAAGTTTGTAATTTATATTAATCTTTAGTTGATACATAAGATTAACATAT	483
QY	495	TCTGTATTCTTCCAAAAA	523
Db	484	TCTGTATTCTTCCAAAAA	512
RESULT 4			
LOCUS	BX091668	519 bp	mRNA linear EST 23-JAN-2003
DEFINITION	BX091668 Soares ovary tumor Nbh07 Homo sapiens cDNA clone		
LOCUS	IMAGE998M041818 ; IMAGE:740523, mRNA sequence.		
ACCESSION	BX091668		
VERSION	BX091668.1	GI:27822555	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 519)		
AUTHORS	Ebert,J., Hell,O., Hennig,S., Neubert,P., Parsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.		
TITLE	Human Unigeneset - RZPD3		
JOURNAL	Unpublished		
COMMENT	Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD: IMAGE998M041818. RZPDLIB: I.M.A.G.E. cDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No. 972) http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, primer sequence: TTTCACACAGGAACACACTATGAC.		
FEATURES			
SOURCE	Location/Qualifiers		
	1..519		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE998M041818 ; IMAGE:740523"		
	/sex="female"		
	/tissue_type="ovarian tumor"		

QY 495 TCTGTATTTCTTCCA 508
Db 481 TCTGTATTTCTTCCA 494

RESULT 6
LOCUS BG249994 962 bp mRNA linear EST 13-FEB-2001
DEFINITION 602362062F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4470662 5', mRNA sequence.
ACCESSION BG249994
VERSION BG249994.1 GI:12759810
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 962)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov
Plate: LLM10288 row: k column: 15
High quality sequence stop: 516.
Location/Qualifiers
1. 962
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4470662"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 334 a 199 c 288 g 141 t
ORIGIN

Query Match 92.2%; Score 492.4; DB 10; Length 962;
Best Local Similarity 99.6%; Pred. No. 2.3e-47;
Matches 504; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 29 GGGGAGAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGTTCATCGCTTCGACAGAA 88
Db 1 GGGGAGAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGTTCATCGCTTCGACAGAA 60

QY 89 CTTACTAGGACGACCTGAGAGAGATTGAGGGAAAGTGTCTGTCTGGCTTCGACAGAC 148
Db 61 CTTACTAGGACGACCTGAGAGAGATTGAGGGAAAGTGTCTGTCTGGCTTCGACAGAC 120

QY 149 GCGATGATACGACGACGACGAGAAATAAACATGCGCCCTTCGCTTCAGTGGAGAAAGGC 208
Db 121 GCGATGATACGACGACGACGAGAAATAAACATGCGCCCTTCGCTTCAGTGGAGAAAGGC 180

QY 209 CACGTGAAGATGCTGCGGCTGGATATTATCACTCACTGTGTAAACACAGATTTCATGCTC 268
Db 181 CACGTGAAGATGCTGCGGCTGGATATTATCACTCACTGTGTAAACACAGATTTCATGCTC 240

QY 269 ATCTATCTGTGTTGGACACTGATCCAGAAACCAACATTGACAGTTGGTGAAGGGGTG 328
Db 241 ATCTATCTGTGTTGGACACTGATCCAGAAACCAACATTGACAGTTGGTGAAGGGGTG 300

QY 329 TTTCACCTTGATGACAGCAATATGCTGTCTTCCGACGGGGCCCTTATTACCGGAAGCTT 388
Db 301 TTTCACCTTGATGACAGCAATATGCTGTCTTCCGACGGGGCCCTTATTACCGGAAGCTT 360

QY 389 CTGTTCAATCCAGCGGCTCTTACGAGAAAGCCGTGTCATGAAAGAAAGAGTTTG 448
Db 361 CTGTTCAATCCAGCGGCTCTTACGAGAAAGCCGTGTCATGAAAGAAAGAGTTTG 419

QY 449 TAATTTATATTAATCTTTAGTTTGTGATTAAGTATTAACATATTTCTGTATTTCTTCCA 508
Db 420 TAATTTATATTAATCTTTAGTTTGTGATTAAGTATTAACATATTTCTGTATTTCTTCCA 479

QY 509 AAAAAAAAAAAAAAAAAAAAAA 534
Db 480 CAAAAAAAAAAAAAAAAAAAAA 505

RESULT 7
LOCUS BF399486/c 510 bp mRNA linear EST 27-NOV-2000
DEFINITION UI-R-CAI-bjb-b-12-0-UI-61 UI-R-CAI Rattus norvegicus cDNA clone
UI-R-CAI-bjb-b-12-0-UI 3', mRNA sequence.
ACCESSION BF399486
VERSION BF399486.1 GI:11384494
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 510)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLY=A=Yes.
Location/Qualifiers
1. 510
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CAI-bjb-b-12-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_id="UI-R-CAI"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CAI library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
BASE COUNT 130 a 131 c 104 g 145 t
ORIGIN

REFERENCE 1 (bases 1 to 487)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM12328 row: a column: 12
High quality sequence stop: 486.

FEATURES
source
Location/Qualifiers

1..487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5576339"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_92"
/note="Organ: testis; Vector: PCMV-SPORT6; Site 1: Nci1;
Site 2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 135 a 103 c 121 g 128 t
ORIGIN

Query Match 90.9%; Score 485.4; DB 12; Length 487;
Best Local Similarity 99.8%; Pred. No. 2.3e-46;
Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

36 AGTAGGGGAGGCGCGTCTCCGCGCGGTGGCTGTATCGCTTCGAGAACCTACTC 95
Db 1 AGTAGGGGAGGCGCGTCTCCGCGCGGTGGCTGTATCGCTTCGAGAACCTACTC 60
QY 96 AGGAGCGCAGCTGAGAGAGTTGAGGAGAAAGTGTCTGCTGGGTTCGACAGCGCATGG 155
Db 61 AGGAGCGCAGCTGAGAGAGTTGAGGAGAAAGTGTCTGCTGGGTTCGACAGCGCATGG 120
QY 156 ATACGTCGACGCGAATAAATCAATGCCCCCTCTGCTCACTGTAAGGCGCAGTGA 215
Db 121 ATACCTGCGCCGCAATAAATCAATGCCCCCTCTGCTCACTGTAAGGCGCAGTGA 180
QY 216 AGATGCTGCGGCTGATATTTATCACTCACTGTAAGCAAGTATTCATGCTCATGTA 275
Db 181 AGATGCTGCGGCTGATATTTATCACTCACTGTAAGCAAGTATTCATGCTCATGTA 240
QY 276 CTGTGTTGGCAGTATACAGAAACCAACATTTGACAGTTGTGAGAGGGGTGTTTCAC 335
Db 241 CTGTGTTGGCAGTATACAGAAACCAACATTTGACAGTTGTGAGAGGGGTGTTTCAC 300
QY 336 TTGGAAGAGAGTGTGCTGCTGCGCAGCGGGGCTTATTTACCGAAGCTTCTGTTC 395
Db 301 TTGGAAGAGAGTGTGCTGCTGCGCAGCGGGGCTTATTTACCGAAGCTTCTGTTC 360
QY 396 ATCCAGCGGTCTTACAGAAAGCTGTGATGAGAAAAAGAGTTTGTATTTT 455
Db 361 ATCCAGCGGTCTTACAGAAAGCTGTGATGAGAAAAAGAGTTTGTATTTT 420
QY 456 ATATTACTTTTATGTTGATTAAGTATTAACATATTTCTGATTTCTCAAAAAA 515
Db 421 ATATTACTTTTATGTTGATTAAGTATTAACATATTTCTGATTTCTCAAAAAA 480
QY 516 AAAAAA 522
Db 481 AAAAAA 487

RESULT 10
BUS66499 526 bp mRNA linear EST 16-SEP-2002
LOCUS BUS66499
DEFINITION AGENCOURT 10397961 NIH_MGC 141 Homo sapiens cDNA clone
IMAGE:6605733 5', mRNA sequence.

ACCESSION BUS66499
VERSION BUS66499.1 GI:22916799
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 526)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM2850 row: d column: 21
High quality sequence stop: 494.

FEATURES
source
Location/Qualifiers

1..526
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6605733"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_id="NIH_MGC_141"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccatcagcgc);
Site 2: SfiI (ggcgctcgccgc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGCAGTGTATCAACGACAGAGCGCATACGCGCGG-3' and
5'-ATCTAGAGCCGAGGCGCGCAATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.2-0.5
kb size fraction (other fractions present in NIH_MGC 142).
Library created in the laboratory of M. Brownstein (NIH,
NIH). Note: this is a NIH_MGC Library."

BASE COUNT 126 a 106 c 135 g 132 t 27 others
ORIGIN

Query Match 90.9%; Score 485.4; DB 13; Length 526;
Best Local Similarity 95.9%; Pred. No. 2.2e-46;
Matches 486; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

23 GAGCTGGGCGAGAGTAGGGGAGGCGGTGCTCCGCGCGGTGGCTGTATCGCTTC 82
Db 4 GAGCTGGGCGAGAGTAGGGGAGGCGGTGCTCCGCGCGGTGGCTGTATCGCTTC 63
QY 83 GCAGAACTTACTAGGAGCGCAGCTAGAGAGAGTTGAGGGAAGTGTGCTGGGTCT 142
Db 64 GCAGAACTTACTAGGAGCGCAGCTAGAGAGAGTTGAGGGAAGTGTGCTGGGTCT 123
QY 143 GCAGAGCGGATGATTAAGTGCAGCGGAGAAATTAACATGCGCTTCTCAAGTGTG 202
Db 124 GCAGAGCGGATGATTAAGTGCAGCGGAGAAATTAACATGCGCTTCTCAAGTGTG 183
QY 203 AAGGCGCAGTGAAGATGCTGCGGCTGATTTATCAACTGATGTAACAGATTTG 262
|||||

Db 184 AAGGCCAGTGAAGATGCTGGCTGATATTAATCACTGATGTAACAACAGTATTC 243
Qy 263 ATGCTCATGATATCTGTGTGGCACTGATACAGAAACCAACATTTGAGTGGGA 322
Db 244 ATGCTCATGATATCTGTGTGGCACTGATACAGAAACCAACATTTGAGTGGGA 303
Qy 323 GGGGTGTTTGACCTGTGACAGCAGTATGCTGTCCGACGGGGCCCTTATTTACCGG 382
Db 304 GGGGTGTTTGACCTGTGACAGCAGTATGCTGTCCGACGGGGCCCTTATTTACCGG 363
Qy 383 AAGCTTCGTTCATCCAGAGGCTCTTACCAAGAAAAAGCTGTGCATGAAAAAGAA 442
Db 364 AAGCTTCGTTCATCCAGAGGCTCTTACCAAGAAAAAGCTGTGCATGAAAAAGAA 423
Qy 443 GTTTGATATTTATTAATCTTTTATGTTAGTACTAGTATTAACATATTTCTGATTT 502
Db 424 GTTTGATATTTATTAATCTTTTATGTTAGTACTAGTATTAACATATTTCTGATTT 483
Qy 503 CTTCCAAAAAAGAAAAAAGAAAAA 529
Db 484 CTTCCAAAAAAGAAAAAAGAAAAA 510

RESULT 11
Bg031757 534 bp mRNA linear EST 24-JAN-2001
LOCUS 602299819P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4394093 5',
DEFINITION mRNA sequence.
ACCESSION Bg031757
VERSION Bg031757.1 GI:12422364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 534)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM10089 row: e column: 06
High quality sequence stop: 446.
Location/Qualifiers
1. 534
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4394093"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="HDH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

BASE COUNT 163 a 108 c 132 g 131 t
ORIGIN

Query Match 90.3%; Score 482.4; DB 10; Length 534;
Best Local Similarity 98.2%; Pred. No. 4.8e-46;
Matches 499; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

Qy 30 GCGAAGAACTAGGAGGCGGTGCTCCGCCGCTGGCGGCTTGATGCTTCGAGAAC 89
|||||

Db 1 GCGAAGAACTAGGAGGCGGTGCTCCGCCGCTGGCGGCTTGATGCTTCGAGAAC 60
Qy 90 CTATCTCAGGACGACGCTGAGAGAGTTGAGGAGAAAGTGTCTGTCTGCTGACAGC 149
Db 61 CTATCTCAGGACGACGCTGAGAGAGTTGAGGAGAAAGTGTCTGTCTGCTGACAGC 120
Qy 150 CGATGATTAACGTGACGACCGGAAATTAACATGCCCCCTTCTGCTTCACTGTGAAAGCC 209
Db 121 CGATGATTAACGTGACGACCGGAAATTAACATGCCCCCTTCTGCTTCACTGTGAAAGCC 180
Qy 210 ACGTGAAGATGCTGGCGCTGGATATTAATCACTCACTGTTAACAACAGTATTCATGCTCA 269
Db 181 ACGTGAAGATGCTGGCGCTGGATATTAATCACTCACTGTTAACAACAGTATTCATGCTCA 240
Qy 270 TCGATCTGTGTTGGCACTGATACCAAGAAACCAACATTTGACAGTGTGTGAGGGGTGT 329
Db 241 TCGATCTGTGTTGGCACTGATACCAAGAAACCAACATTTGACAGTGTGTGAGGGGTGT 300
Qy 330 TTGCACTTGTGACAGCAGTATGCTGTCTTCCGACGGGGCCCTTATTTACCGAAGCTTC 389
Db 301 TTGCACTTGTGACAGCAGTATGCTGTCTTCCGACGGGGCCCTTATTTACCGAAGCTTC 360
Qy 390 TGTTCATCCGACGGGCTTACCAAGAAAGCTGTGATGAAAGAAAGTTTGT 449
Db 361 TGTTCATCCGACGGGCTTACCAAGAAAGCTGTGATGAAAGAAAGTTTGT 420
Qy 450 AATTTATATTAATCTTTTATGTTGATTAAG--TATTAACATATTTCTGATTTCTTC 506
Db 421 AATTTATATTAATCTTTTATGTTGATTAAGTATTTAAACATATTTCTGATTTCTTC 480
Qy 507 CAAAAAAGAAAAAAGAAAAAAGAAAAA 534
Db 481 CAAAAAAGAAAAAAGAAAAAAGAAAAA 508

RESULT 12
BX422104 671 bp mRNA linear EST 13-MAY-2003
LOCUS BX422104 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
DEFINITION clone CS0DH007YB16 5'-PRIME, mRNA sequence.
ACCESSION BX422104
VERSION BX422104.1 GI:30647202
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 671)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8312.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DH007DA08QPL&cluster=8312.f. Contact :
Feng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DH007DA08QPL.
Location/Qualifiers
1. 671
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DH007YB16"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed

with a NotI-oligo (dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

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BASE COUNT      154 a      113 c      133 g      249 t      22 others
ORIGIN

Query Match      89.0%; Score 475; DB 13; Length 671;
Best Local Similarity 98.0%; Pred. No. 2.8e-45;
Matches 486; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

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DB 65 GGATGGAGGCGGTGCTCCGCGCGGTGCTTATCGCTTCCAGAACCTACTCA 123
QY 97 GGAGGCGAGTGAAGAGTTGAGGAGAAAGTGTGCTGCTGCTGCTGCTGCTGCA 156
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DB 544 AAAAAAAAAAAAAA 559

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DEFINITION      clone CS0DH007YB16 5-PRIME, mRNA sequence.
ACCESSION      BX464689
VERSION      BX464689.1 GI:31033656
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLES      1 (bases 1 to 1201)
JOURNAL      Full-length cDNA libraries and normalization
COMMENT      Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8312.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS1DH002ZF11QPI&cluster=8312.f. Contact :
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Peng Liang Email: liang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS1DH002ZF11QPI.
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/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
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double-strand cDNA was digested with Not I and EcoRV
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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BASE COUNT      302 a      298 c      248 g      180 t      173 others
ORIGIN
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Query Match 88.8%; Score 474.4; DB 13; Length 1201;
Best Local Similarity 98.0%; Pred. No. 2.2e-45;
Matches 478; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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DB 91 GGAGGCGAGTGAAGAGTTGAGGAGAAAGTGTGCTGCTGCTGCTGCTGCTGCA 150
QY 157 TAAAGTGCAGCCGAAATTAACAATCGCCCTTCTGCTTCAAGTGTGAAGGCCA 216
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QY 217 GATGCTGCGGCTGATATTATCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 276
DB 211 GATGCTGCGGCTGATATTATCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270
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DB 271 TGTGTTGGAGCTGATATCAAGAACCAACATTTGAGGAGGCTTGTGCACT 330
QY 337 TGTGACAGCAGTATGCTGTCTTCCGAGCGGGCCCTTATTTACCGAAGCTTCT 396
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QY 397 TCCGAGGCGTCTTACCAAGAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 456
DB 391 TCCGAGGCGTCTTACCAAGAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 450
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QY 517 AAAAAAA 524
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LOCUS      BU565721
DEFINITION      AGENCOURT_10401193 NIH_MGC_141 Homo sapiens cDNA clone
ACCESSION      BU565721
VERSION      BU565721.1 GI:22916011
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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Db 301 TGACAGCAGTATGCTGTCTTGCCGACGGGGCCCTTATTACCGGAAGCTTCTGTTCAATC 360
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Job time : 2077 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 02:47:22 ; Search time 77 seconds
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Searched: 569978 seqs, 220691566 residues 1139956

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

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1	493.4	92.4	515	US-09-599-360B-29	Sequence 29, Appl
2	486.6	91.1	504	US-09-149-476-98	Sequence 98, Appl
3	478.6	89.6	506	US-09-149-476-252	Sequence 252, Appl
4	466.8	87.4	500	US-09-663-600A-53	Sequence 53, Appl
5	465.8	87.2	526	US-09-220-132-164	Sequence 164, Appl
6	411.4	77.0	413	US-09-663-600A-147	Sequence 147, Appl
7	321.8	60.3	669	US-09-599-360B-70	Sequence 70, Appl
8	272	50.9	392	US-09-385-982-95	Sequence 95, Appl
9	50.4	9.4	1582	US-08-545-196B-10	Sequence 10, Appl
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11	46.8	8.8	770	US-08-865-297-5	Sequence 5, Appl
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21	44.2	8.3	581	US-08-834-306-22	Sequence 22, Appl
22	44.2	8.3	581	US-08-993-674A-22	Sequence 22, Appl
23	44.2	8.3	581	US-09-256-976-22	Sequence 22, Appl
24	44.2	8.3	1033	US-09-610-185C-3	Sequence 3, Appl
25	43.6	8.2	1544	US-09-187-999-14	Sequence 14, Appl
26	43	8.1	2589	US-08-569-749-1	Sequence 1, Appl
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37	42	7.9	2025	US-09-149-476-316	Sequence 316, Appl
38	42	7.9	2346	US-09-149-476-193	Sequence 193, Appl
39	41.8	7.8	742	US-07-847-010-12	Sequence 12, Appl
40	41.8	7.8	1465	US-09-573-906-1	Sequence 1, Appl
41	41.6	7.8	1443	US-09-573-906-1	Sequence 1, Appl
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43	41.4	7.8	511	US-09-328-475C-196	Sequence 196, Appl
44	41.4	7.8	5852	US-07-867-106C-2	Sequence 2, Appl
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ALIGNMENTS

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RESULT 1
US-09-599-360B-29
Sequence 29, Application US/09599360B
Patent No. 6548633
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET 050CP3
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 29
LENGTH: 515
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 144..440
NAME/KEY: sig_peptide
LOCATION: 144..287
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.10
NAME/KEY: polyA_signal
LOCATION: 457..462
NAME/KEY: polyA_site
LOCATION: 500..515
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a, g, c or t
US-09-599-360B-29
Query Match 92.4%; Score 493.4; DB 4; Length 515;
Best Local Similarity 99.4%; Pred. No. 1.1e-116;
Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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DB 8 GGGAGCCGAGCTGGGAGGAAGTAAGGAGGCGGCTCCGCGGCTGGCGTCTGCT 66
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RESULT 2
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 Sequence 98 Application US/091149476.
 Patent No. 6420526
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 166 Human Secreted proteins
 FILE REFERENCE: P2002p1
 CURRENT APPLICATION NUMBER: US/09/149,476
 CURRENT FILING DATE: 1998-09-08
 EARLIER APPLICATION NUMBER: PCT/US98/04493
 EARLIER FILING DATE: 1998-03-06
 EARLIER APPLICATION NUMBER: 60/040,162
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/040,333
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/038,621
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 EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/048,964
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/057,650
 EARLIER FILING DATE: 1997-09-05
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 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/057,669
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/049,610
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/061,060
 EARLIER FILING DATE: 1997-10-02

Query Match 91.1%; Score 486.6; DB 4; Length 504;
 Best Local Similarity 99.0%; Pred. No. 5.9e-115;
 Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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 DB 1 CCGAGCTGGGCGAGAGTAGGGGAGGGGCGGTCTCCGCCGCGGTGGCGGTGCTATCGCT 59

QY 81 TCGCAGAACTTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGT 140
 DB 60 TCGCAGAACTTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGT 119

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RESULT 3
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 Sequence 252, Application US/09149476
 Patent No. 6420526
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 186 Human Secreted proteins
 FILE REFERENCE: P2002P1
 CURRENT APPLICATION NUMBER: US/09/149,476
 EARLIER FILING DATE: 1998-09-08
 EARLIER APPLICATION NUMBER: PCT/US98/04493
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EARLIER	APPLICATION NUMBER: 60/041,597
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,592
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,581
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,584
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,500
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,587
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,492
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,598
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,613
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,582
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,596
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,612
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,632
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/041,600
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/043,560
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,568
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,314
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,565
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,311
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,671
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,674
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,669
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,312
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043,313

[illegible]

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EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Query Match 89.6%; Score 478.6; DB 4; Length 506;
Best Local Similarity 97.4%; Pred. No. 6.4e-113;
Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

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37 GTAGGAGAGGCGGCTGCTCCCGCGGCGGCTGCTATGCTTCCGAACTACTCA 96
2 GCAGGATTTGGCCGAGGCCGCCCGGCGGCTGCTATGCTTCCGAACTACTCA 61
97 GGCAGCAGCTGAGAGAGTGAAGGAAAGTGTGCTGGTCTGCTGAGCGGATGGA 156
62 GGCAGCAGCTGAGAGAGTGAAGGAAAGTGTGCTGGTCTGCTGAGCGGATGGA 121
157 TAAAGTGAAGCGGAAATTAACAATCGCCCTTCTGCTTCAAGTGAAGCGCACTGAA 216
122 TAAAGTGAAGCGGAAATTAACAATCGCCCTTCTGCTTCAAGTGAAGCGCACTGAA 181
217 GATGCTGGCTGATATTAATCACTCACTGCTGAACAACATGATTCATGCTCATGATC 276
182 GATGCTGGCTGATATTAATCACTCACTGCTGAACAACATGATTCATGCTCATGATC 241
277 TGTGTTGGCACTGATATCAACAGAAACCAACATGACAGTTGGTGAAGGGGTTGCACT 336
242 TGTGTTGGCACTGATATCAACAGAAACCAACATGACAGTTGGTGAAGGGGTTGCACT 301
337 TGTGACAGCACTATGCTGCTTGGCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAA 396
302 TGTGACAGCACTATGCTGCTTGGCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAA 361
397 TCCCAAGCGGCTCTTAACGAAAAAGCTGTGCAATGAAAAAAGAGTTTGTAAATTTTA 456
362 TCCCAAGCGGCTCTTAACGAAAAAGCTGTGCAATGAAAAAAGAGTTTGTAAATTTTA 421
```

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457 TATTACTTTTACTGTTGATCTAAGTATTAACATATTTCTGATTTCTCCAAAAAAA 516
422 TATTACTTTTACTGTTGATCTAAGTATTAACATATTTCTGATTTCTCCAAAAAAA 481
517 AAAAAAAAAAAAAAAAAA 533
482 AAAAAAAAAAAAAAAAAA 498

RESULT 4
US-09-663-600A-53
Sequence 53, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleret, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 53
LENGTH: 500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 199..288
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.59999990463257
NAME/KEY: polyA_signal
LOCATION: 464..469
NAME/KEY: polyA_site
LOCATION: 489..500
NAME/KEY: misc_feature
LOCATION: 197..412
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA429945
OTHER INFORMATION: est
NAME/KEY: misc_feature
LOCATION: 425..488
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA429945
NAME/KEY: misc_feature
LOCATION: 197..412
OTHER INFORMATION: homology
OTHER INFORMATION: id: AA455042
NAME/KEY: misc_feature
LOCATION: 61..195
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? NAME/KEY: misc feature
? LOCATION: 40..195
? OTHER INFORMATION: homology
? OTHER INFORMATION: id :W19506
? OTHER INFORMATION: est
? NAME/KEY: misc feature
? LOCATION: 9..10,12
? OTHER INFORMATION: n=a, g, c or t
? US-09-663-600A-53

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Oy	23	GAGCTGGGCGGAAGTATGGGAGAGGGCGGTGCTCCGCGCGGGTGGCGG--TTGGTATCGGCT	81
Db	2	GAGCTGNNCNSAAGTAGGGGAGGGCGGTGCTCCGCMGGGTGGCGGHTGCTATCGGCT	61
Oy	82	CGCGAAGCTTACTAGGCGACCCAGCTGAGAGAGTTAGGGGAAGTGTCTGCTGGGTC	141
Db	62	CGCGAAGCTTACTAGGCGACCCAGCTGAGAGAGTTAGGGGAAGTGTGCTGGGTC	121
Oy	142	TGCAGACGGCATGTGATTAACGTGACGCCGAATAATAACATGCGCCCTTCTGCTTCAGTGT	201
Db	122	TGCAGACGGCATGTGATTAACGTGACGCCGAATAATAAATGCGCCCTTCTGCTTCAGTGT	181
Oy	202	GAAGGCCACGTGA--AGATGCTGCGGCTGTGATATTATCACTCACTGTTAACACAGTAT	260
Db	182	GAAGGCCACGTGAVAGATGCTGCGGGCTGTGATATTATCACTCACTGTTAACACAGTAT	241
Oy	261	TCATGCTCATGTATCTGTGTTGGCACTGATACAGAAACCAACATTTGACAGTTGGTG	320
Db	242	TCATGCTCATGTATCTGTGTTGGCACTGATACAGAAACCAACATTTGACAGTTGGTG	301
Oy	321	GAGGGGTGTTGCACTGTGTGACAGACAGTATGCTGTCTTGGCGAGCGGCCCTTATTATACC	380
Db	302	GAGGGGTGTTGCACTGTGTGACACAGATATCTGTCTTGGCGAGCGGCCCTTATTATACC	361
Oy	381	GGAGGCTTCTGTGTAATCCGAGGGTCTTACCGAATAAAGCTGTGATGAAAAAANAAG	440
Db	362	GGAGGCTTCTGTGTAATCCAGCGGTCTTACCGAATAAAGCTGTGATGAAAAAANAAG	421
Oy	441	AAGTTTGTATTTTATATATTAATCTTTTATAGTTTGAATACTAAGTATTAACATATTTTCTGTA	500
Db	422	AAGTTTGTATTTTATATATTAATCTTTTATAGTTTGAATACTAAGTATTAACATATTTCTGTA	481
Oy	501	TTCTTCCAAAAAANAANA 519	
Db	482	TTCTTCCAAAAAANAANA 500	

ORGANISM: *Homo sapiens*
FEATURE:


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ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 140..595
NAME/KEY: sig_peptide
LOCATION: 140..442
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.10
OTHER INFORMATION: seq VFMLIVSLALIP/ET
NAME/KEY: polyA_signal
LOCATION: 630..635
NAME/KEY: polyA_site
LOCATION: 655..669
US-09-599-3608-70

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Query Match      60.3%; Score 321.8; DB 4; Length 669;
Best Local Similarity 75.6%; Pred. No. 6.2e-73;
Matches 504; Conservative 0; Mismatches 2; Indels 161; Gaps 2;

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QY 15 GTGAAGCCGAGCTGGGCGAGAGTAGGGGAGGGCGGTCTCCGCGCGGTGGCGGTGCT 74
DB 5 GGAAGCCGAGCTGGGCGAGAGTAGGGGAGGGCGGTCTCCGCGCGGTGGCGGTGCT 64
QY 75 ATGCGCTTGGCAGAACTTACTAGGCGAGCCAGCTGAGAAAGTTGAGGAAAGTGTGCTG 134
DB 65 ATCCCTTGGCAGAACTTACTAGGCGAGCCAGCTGAGAAAGTTGAGGAGG--ATTGCTGTG 122
QY 135 CTGGGTCTGCGAGAGCGGATGATTAACGTGCGAGCGGAAATTAACATGCGCCCTTCTGCT 194
DB 123 CTGGGTCTGCGAGAGCGGATGATTAACGTGCGAGCGGAAATTAACATGCGCCCTTCTGCT 182
QY 195 TCAGTGTGAAAGGCGCAGTGAAGTGTGCGGCTG----- 229
DB 183 TCAGTGTGAAAGGCGCAGTGAAGTGTGCGGCTGCGCACTAAGTGAACATCTATGACCT 242
QY 230 ----- 229
DB 243 TTTTATCATGCGCAAGAGCCCTGAAACCATATATTGTTATCATGATTTGAAGTCAAG 302
QY 230 ----- 229
DB 303 TTATCTATTTTTCTACTTTTATATATGTACTGACCTTGATGATTAAGTGAAGTGTAT 362
QY 230 ----- 275
DB 363 TTGGCCTTGGCTGATTTATTAACACTGACTGATGAACAGTATTAATGCTCATCGTAT 422
QY 276 CTGTGTGGCACTGATTAACCAAGAACCAACATTTGACAGTTGGTGGAGGGGTGTTGCA 335
DB 423 CTGTGTGGCACTGATTAACCAAGAACCAACATTTGACAGTTGGTGGAGGGGTGTTGCA 482
QY 336 TTGTGACGACGATATGCTGTCTGCGAGGGGGCCCTTATTACCGGAAGCTTCTGTTCA 395
DB 483 TTGTGACGACGATATGCTGTCTGCGAGGGGGCCCTTATTACCGGAAGCTTCTGTTCA 542
QY 396 ATCCAGCGGTCTTACCAAGAAAGCCTGTGATGAAAGAAAGAAAGTTTGTATTTT 455
DB 543 ATCCAGCGGTCTTACCAAGAAAGCCTGTGATGAAAGAAAGAAAGTTTGTATTTT 602
QY 456 ATATTACTTTTGTAGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAAAA 515
DB 603 ATATTACTTTTGTAGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAAAA 662
QY 516 AAAAAA 522
DB 663 AAAAAA 669

```

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RESULT 8
US-09-385-982-95
Sequence 95, Application US/09385982
Patent No. 6262334
GENERAL INFORMATION:

```

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APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCNDA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
EARLIER FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 344
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 95
LENGTH: 392
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(392)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-95

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Query Match      50.3%; Score 272; DB 3; Length 392;
Best Local Similarity 95.5%; Pred. No. 2.4e-60;
Matches 297; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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QY 226 GCTGGATATTATGACATCTGATGTAACAGATTTCAATGCTATCTGTGTTGGC 285
DB 43 GCTGGATATTATGACATCTGATGTAACAGATTTCAATGCTATCTGTGTTGGC 102
QY 286 ACTGATACGAGAAACCAACATTTGACAGTTGTGAGGGGTGTTGCACTTGTGACAGC 345
DB 103 ACTGATACGAGAAACCAACATTTGACAGTTGTGAGGGGTGTTGCACTTGTGACAGC 162
QY 346 AGTATGCTGTCTGCGAGCGGGCCCTTATTACCGGAAGCTTGTTCATCCACGG 405
DB 163 AGTATGCTGTCTGCGAGCGGGCCCTTATTACCGGAAGCTTGTTCATCCACGG 222
QY 406 TCCCTACGAGAAAGCGTGTGATG-AAAAAAGAGTTTGTATTTATTTACTT 464
DB 223 TCCCTACGAGAAAGCGTGTGATGAAAAAAGAGTTTGTATTTATTTACTT 282
QY 465 TTT-AGTTGATCTAAGTATTAACATATTTCTGATTTCTTCCAAAAAAA 523
DB 283 NTTAAGTTGATCTAAGTATTAACATATTTCTGATTTCTTCCAAAAAAA 342
QY 524 AAAAAA 534
DB 343 TNAANTTANAA 353

```

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RESULT 9
US-08-545-196B-10
Sequence 10, Application US/08545196B
Patent No. 6080577
GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MÜNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/545,196B
/ FILING DATE: 19-OCT-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PARACI, C. J.
/ REGISTRATION NUMBER: 32,350
/ REFERENCE/DOCKET NUMBER: 2121-110P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 205-8000
/ TELEFAX: (703) 205-8050
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1582 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: CDNA
/
/ US-08-545-196B-10
/
Query Match          9.4%; Score 50.4; DB 3; Length 1582;
Best Local Similarity 71.7%; Pred. No. 0.0012;
Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Oy 443 GTTTGTATTTATATTAATCTTTTGTAGTTGATCTAGATTAACATATTTCTGTAT 502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1427 GTACTGTTTTTTCTATCTCTCATATGTTTAAAGTATATATAATTTAATTTT 1486
/
Oy 503 CTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1487 TTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1518
/
RESULT 10
/ US-08-545-196B-12
/ Sequence 12, Application US/08545196B
/ Patent No. 6080577
/
/ GENERAL INFORMATION:
/ APPLICANT: MELKI, JUDITH
/ APPLICANT: MINNICH, ARNOLD
/ TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
/ TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
/ STREET: PO BOX 747
/ CITY: FALLS CHURCH
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22040-0747
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/545,196B
/ FILING DATE: 19-OCT-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PARACI, C. J.
/ REGISTRATION NUMBER: 32,350
/ REFERENCE/DOCKET NUMBER: 2121-110P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 205-8000
/ TELEFAX: (703) 205-8050
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1582 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-545-196B-12

Query Match          9.4%; Score 50.4; DB 3; Length 1582;
Best Local Similarity 71.7%; Pred. No. 0.0012;
Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY      443 GTTTGTAATTTTACTTTAGTTGATACTAAGTATTAAACATATTCGTATT 502
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1427 GTACTGTTTTTTCTACTCTCTATATGTTTAAAAGTATATATATAATTTAATTTT 1486

QY      503 CTCCAAAAAAAAAAAAAAAAAAAAAA 534
        || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1487 TTTTAAAAAAAAAAAAAAAAAAAAAA 1518

RESULT 11
US-08-865-297-5
; Sequence 5, Application US/08865297
; Patent No. 6010853
; GENERAL INFORMATION:
; APPLICANT: Prasad V.S. Kanteli, Zhaohui Ao, and Stuart F.
; APPLICANT: Schlossman
; TITLE OF INVENTION: The Siva Genes, No. 6010853el Genes Involved in
; TITLE OF INVENTION: CPD2-Mediated Apoptosis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,297
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: PFN-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO.: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..612
US-08-865-297-5

Query Match          8.8%; Score 46.8; DB 3; Length 770;
Best Local Similarity 61.5%; Pred. No. 0.0072;
Matches 75; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      413 CAGAAAAGCCCTGCATGAAGAAAGATTTGTATTTATTTACTTTTAGCTTT 472
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      628 CAGCACAAGATGTTCACTCAAAGAAGAGAAAGTGCTTTTATATGTATGTTTATA 687

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QY 473 GATACGATGATTAACATATTTCTGATTCCTCCAAAAA 532
| | | | |
DB 688 CCGGTACAGGATGATTAACCTCTTATATTTCCAAAAA 747
| | | | |
QY 533 AA 534
| |
DB 748 AA 749

RESULT 12

US-08-890-865A-2
; Sequence 2, Application US/08890865A
; Patent No. 6307019
; GENERAL INFORMATION:
; APPLICANT: Constantini, Franklin
; APPLICANT: Zeng, Li
; TITLE OF INVENTION: AXIN GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,865A
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/54249
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3761 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-890-865A-2

Query Match 8.6%; Score 45.8; DB 4; Length 3761;
Best Local Similarity 67.0%; Pred. No. 0.025;
Matches 65; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 438 AAGAGTTTGTATTTATATTTAGTTTGATGATTAACATATTTCT 497
| | | | |
DB 3662 AATGACTGTGACATTAATCTTTCAAGGTAATGATTAATGAATATTAACGTTT 3721
| | | | |
QY 498 GTATTTCCAAAAA 534
| | | | |
DB 3722 TGAACCTTCCAAAAA 3758
| | | | |

RESULT 13
5194596-16
; Patent No. 5194596
; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDES, JOHN
; C. MITCHELL, RICHARD L.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/450,883

; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:16:
; LENGTH: 961
; 5194596-16

Query Match 8.4%; Score 45; DB 6; Length 961;
Best Local Similarity 63.3%; Pred. No. 0.023;
Matches 69; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 426 TCGATGAAAAAAGAGTTTGTATTTATTTACTTTTGTGATGATTAAGTATT 485
| | | | |
DB 852 TACATTTA 911
| | | | |
QY 486 AACATATTTCTGATTCCTCCAAAAA 534
| | | | |
DB 912 TATTAATATATATATTTCTTTTAAAAA 960
| | | | |

RESULT 14

5219739-16
; Patent No. 5219739
; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDES,
; JOHN C.; MITCHELL, RICHARD L.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BVGFI20 AND
; BVGFI 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
; VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVGFI20 AND BVGFI21
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/559,041
; FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 450,883
; FILING DATE: 14-DEC-1989
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:16:
; LENGTH: 961
; 5219739-16

Query Match 8.4%; Score 45; DB 6; Length 961;
Best Local Similarity 63.3%; Pred. No. 0.023;
Matches 69; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 426 TCGATGAAAAAAGAGTTTGTATTTATTTACTTTTGTGATGATTAAGTATT 485
| | | | |
DB 852 TACATTTA 911
| | | | |
QY 486 AACATATTTCTGATTCCTCCAAAAA 534
| | | | |
DB 912 TATTAATATATATTTCTTTTAAAAA 960
| | | | |

RESULT 15
US-09-205-258-64
; Sequence 64, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 64
LENGTH: 588
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (565)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (566)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-64

Query Match 8.4%; Score 44.6; DB 4; Length 588;
Best Local Similarity 71.1%; Pred. No. 0.024;
Matches 59; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 452 TTTTATTTACTTTTGTGTTGATTAAGTATTAAACATATTCTGTATTTCCAAA 511
|||||
Db 440 TTTTATTTCTGTGGGCTCACCCCAAGTATTAAAGTATTGTAATTCAAAA 499
|||||
QY 512 AAAAAAAAAAAAAAAAAAAAAA 534
|||||
Db 500 AAAAAAAAAAAAAAAAAAAAAA 522
|||||

Search completed: January 31, 2004, 04:11:09
Job time : 79 secs

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Db 61 CGGTGGCGGTGCTACCTTCGACAGAACTTACAGGACGACGAGTGAAGAGTTGAG 120
Qy 121 GGAAGTCTGCTGCTGGGCTCTGACAGCGGATGATTAAGCCGAAATTAACA 180
Db 121 GGAAGTCTGCTGCTGGGCTCTGACAGCGGATGATTAAGCCGAAATTAACA 180
Qy 181 TCGCCCTTCTGCTTCACTGTAAGGCGACGTGAAGTGTGGCTGATATTATCAA 240
Db 181 TCGCCCTTCTGCTTCACTGTAAGGCGACGTGAAGTGTGGCTGATATTATCAA 240
Qy 241 CTCCTGTGTAACAAGTATTCATGCTCATGTATCTGTGTGGCACTGATACCAAAAC 300
Db 241 CTCCTGTGTAACAAGTATTCATGCTCATGTATCTGTGTGGCACTGATACCAAAAC 300
Qy 301 CACAACATTCAGAGTTGGTGAAGGGGTGTGCACTTGACAGCAAGATGCTGCTTGC 360
Db 301 CACAACATTCAGAGTTGGTGAAGGGGTGTGCACTTGACAGCAAGATGCTGCTTGC 360
Qy 361 CGACGGGCGCTTATTTACCGGAAGCTTCTGTCAATCCAGCGGCTCTTACCAAAAA 420
Db 361 CGACGGGCGCTTATTTACCGGAAGCTTCTGTCAATCCAGCGGCTCTTACCAAAAA 420
Qy 421 GCCTGTGATGAAAAAGAGTTTGTATTTATTTATTTTATTTTATTTTATTTTAA 480
Db 421 GCCTGTGATGAAAAAGAGTTTGTATTTATTTATTTTATTTTATTTTATTTAA 480
Qy 481 GTATTAAACATATTTCTGTATTTCTTCCAAAAAATTTTATTTTATTTTATTTTAA 534
Db 481 GTATTAAACATATTTCTGTATTTCTTCCAAAAAATTTTATTTTATTTTATTTTAA 534
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RESULT 2

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US-10-119-428-14
; Sequence 14, Application US/10119428
; Publication No. US20030165881A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Wehtman, Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhou, Ping
; APPLICANT: Zhao, Qiong A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030165881A1el Nucleic Acids and
; FILE REFERENCE: 789CIP2
; CURRENT APPLICATION NUMBER: US/10/119,428
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: pc_fl_genes version 1.0
; SEQ ID NO 14
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (236)..(535)
US-10-119-428-14
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Query Match 95.4%; Score 509.4; DB 13; Length 817;
Best Local Similarity 99.8%; Pred. No. 1.4e-116;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 15 GTGAAGCCAGCTGGGCGAAGTAAGGAGGCGGTCTCCGCCGCGTGGCGTTGCT 74
Db 99 GGAAGCCAGCTGGGCGAAGTAAGGAGGCGGTCTCCGCCGCGTGGCGTTGCT 158
Qy 75 ATGCTTCCGAGAACTTACTCAGCGAGCCGCTGAGAAAGTTGAGGGAAGTCTGCT 134
Db 159 ATGCTTCCGAGAACTTACTCAGCGAGCCGCTGAGAAAGTTGAGGGAAGTCTGCT 218
Qy 135 CTGGGTCTGAGAGCGGATGATTAAGTGAAGCCGAAATTAACAATCGCCCTTCTGCT 194
Db 219 CTGGGTCTGAGAGCGGATGATTAAGTGAAGCCGAAATTAACAATCGCCCTTCTGCT 278
Qy 195 TCAAGTGAAGGCGCAGTGAAGATGCTGGGCTGATATTATCACTCACTGTAACAA 254
Db 279 TCAAGTGAAGGCGCAGTGAAGATGCTGGGCTGATATTATCACTCACTGTAACAA 338
Qy 255 CAGTATTCATGCTCATGCTATCTGTGTGGCACTGATACCAAGAAACCAAACTTGA 314
Db 339 CAGTATTCATGCTCATGCTATCTGTGTGGCACTGATACCAAGAAACCAAACTTGA 398
Qy 315 TTGGTGAAGGGGTGTGTCATCTGTGACAGACAGATAGCTGCTTGGCGAGCGGGCCTT 374
Db 399 TTGGTGAAGGGGTGTGTCATCTGTGACAGACAGATAGCTGCTTGGCGAGCGGGCCTT 458
Qy 375 TTACCGGAAGCTTCTGTCAATCCAGCGGCTCTTACCAAAAAAGCTGTGCATGAAA 434
Db 459 TTACCGGAAGCTTCTGTCAATCCAGCGGCTCTTACCAAAAAAGCTGTGCATGAAA 518
Qy 435 AAAAAGAGTTTGTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTAA 494
Db 519 AAAAAGAGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 578
Qy 495 TCTGTATTTCTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 525
Db 579 TCTGTATTTCTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 609
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RESULT 3

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US-10-291-172-13
; Sequence 13, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 13
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)..(430)
US-10-291-172-13
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Query Match 94.9%; Score 507; DB 12; Length 655;
Best Local Similarity 100.0%; Pred. No. 5.1e-116;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 AGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTCTCGCCGCGGTGCGGTCTATCG 78
|
|
|
Db 1 AGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTCTCGCCGCGGTGCGGTCTATCG 60
|
|
|
QY 79 CTTCGCAAACTTACTAGGACGACGACGACGACGACGACGACGACGACGACGACGACG 138
|
|
|
Db 61 CTTCGCAAACTTACTAGGACGACGACGACGACGACGACGACGACGACGACGACGACG 120
|
|
|
QY 139 GTTCGCAAGGCGGATGATACGTCAGCGGAAATATAATCATGCGCCCTTCTGCTCAG 198
|
|
|
Db 121 GTTCGCAAGGCGGATGATACGTCAGCGGAAATATAATCATGCGCCCTTCTGCTCAG 180
|
|
|
QY 199 TGTGAAGGCGGACGTCGAAGATGTCGCGCTGATATTTATCACTCATGTGAACAAGT 258
|
|
|
Db 181 TGTGAAGGCGGACGTCGAAGATGTCGCGCTGATATTTATCACTCATGTGAACAAGT 240
|
|
|
QY 259 ATTCTATCTCATCTATCTATCTGTTGGCACTGATACCAAAACCAACATTGACAGTTGG 318
|
|
|
Db 241 ATTCTATCTCATCTATCTATCTGTTGGCACTGATACCAAAACCAACATTGACAGTTGG 300
|
|
|
QY 319 TGAAGGGGTGTTGCACTTGTGACAGAGATGCTGTCCGACGCGGCGCTTATTTA 378
|
|
|
Db 301 TGAAGGGGTGTTGCACTTGTGACAGAGATGCTGTCCGACGCGGCGCTTATTTA 360
|
|
|
QY 379 CCGGAAGCTTCTGTTCAATCCGACGCGTCTTACCAAGAAAAAGCTGTGATGAAGAAAA 438
|
|
|
Db 361 CCGGAAGCTTCTGTTCAATCCGACGCGTCTTACCAAGAAAAAGCTGTGATGAAGAAAA 420
|
|
|
QY 439 AGAAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 498
|
|
|
Db 421 AGAAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 480
|
|
|
QY 499 TATCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 525
|
|
|
Db 481 TATCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 507
|
|
|

RESULT 4

US-10-106-698-1927
; Sequence 1927, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT FILING DATE: US/10/106,698
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1927
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (514)..(514)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1927

Query Match 93.1%; Score 497.2; DB 15; Length 558;
Best Local Similarity 98.4%; Pred. No. 1,3e-113;
Matches 499; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 TGAAGCCGAGCTGGCGGAGAAAGTAGAGGAGGCGGTCTCGCCGCGGTGCGGTGCTGA 75
|
|
|
Db 11 TGAAGYSSGAGCTGGCGGAGAAAGTAGAGGAGGCGGTCTCGCCGCGGTGCGGTGCTGA 70
|
|
|

QY 76 TCGCTTCGAGAACTTACTCAGGACGACGTCGAGAAAGTTGAGGAAAGTCTGCTGC 135
|
|
|
Db 71 TCGCTTCGAGAACTTACTCAGGACGACGTCGAGAAAGTTGAGGAAAGTCTGCTGC 130
|
|
|
QY 136 TGGGTCTGCAGAGCGCATGATTAACCTGACCGGAAATATAATCATGCGCCCTTCTGCTT 195
|
|
|
Db 131 TGGGTCTGCAGAGCGCATGATTAACCTGACCGGAAATATAATCATGCGCCCTTCTGCTT 190
|
|
|
QY 196 CAGTGTGAAGGCGGACGATGAGATGTCGCGGCTGATATTTATCACTCATGTGAACAAC 255
|
|
|
Db 191 CAGTGTGAAGGCGGACGATGAGATGTCGCGGCTGATATTTATCACTCATGTGAACAAC 250
|
|
|
QY 256 AGTATTCATCTCATCTATCTGTTGGCACTGATACCAAAACCAACATTGACAGT 315
|
|
|
Db 251 AGTATTCATCTCATCTATCTGTTGGCACTGATACCAAAACCAACATTGACAGT 310
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|
|
QY 316 TGGTGAAGGGGTGTTGCACTTGTGACAGAGATGCTGTCCGACGCGGCGCTTAT 375
|
|
|
Db 311 TGGTGAAGGGGTGTTGCACTTGTGACAGAGATGCTGTCCGACGCGGCGCTTAT 370
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|
|
QY 376 TTAACCGGAGCTTCTGTTCAATCCGACGCGTCTTACCAAGAAAAAGCTGTGATGA 435
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|
|
Db 371 TTAACCGGAGCTTCTGTTCAATCCGACGCGTCTTACCAAGAAAAAGCTGTGATGA 430
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|
|
QY 436 AAAAGAGTTTGTAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 495
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|
|
Db 431 AAAAGAGTTTGTAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 490
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|
|
QY 496 CTGATTTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTT 522
|
|
|
Db 491 CTGATTTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTT 517
|
|
|

RESULT 5

US-09-809-391-98
; Sequence 98, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT FILING DATE: US/09/809,391
; PRIOR APPLICATION NUMBER: 2001-03-16
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-98

Query Match 91.1%; Score 486.6; DB 11; Length 504;
Best Local Similarity 99.0%; Pred. No. 5.2e-111;
Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 21 CCGAGCTGGGCGGAGAACTAGAGGAGGCGGTCTCGCCGCGGTGCGGTGCTATGCT 80
|
|
|
Db 1 CCGAGCTGGGCGGAGAACTAGAGGAGGCGGTCTCGCCGCGGTGCGGTGCTATGCT 59
|
|
|
QY 81 TCGCAGAACTTACTCAGGACGACGTCGAGAAAGTTGAGGAAAGTCTGCTGCGGT 140
|
|
|
Db 60 TCGCAGAACTTACTCAGGACGACGTCGAGAAAGTTGAGGAAAGTCTGCTGCGGT 119
|
|
|
QY 141 CTGCAAGCGGATGATTAACGTCGACGCGGAAATATAATCATGCGCCCTTCTGCTCA 200
|
|
|
Db 120 CTGCAAGCGGATGATTAACGTCGACGCGGAAATATAATCATGCGCCCTTCTGCTCA 179
|
|
|
QY 201 TGAAGGCCACGTCGAATATCTGCGGTGATTTATCACTCATGTGAACAACGATAT 260
|
|
|
Db 180 TGAAGGCCACGTCGAATATCTGCGGTGATTTATCACTCATGTGAACAACGATAT 239
|
|
|

Qy 261 TCATGCTCATGTAATCTGTGTGGCATGATACCAAGAAACCAACATGACATTGGTG 320
Db 240 TCATGCTCATGTAATCTGTGTGGCATGATACCAAGAAACCAACATGACATTGGTG 299
Qy 321 GAGGGGTTTGGCATCTGTGACAGATATCTGTGGAGGGGGCCCTTATTTACC 380
Db 300 GAGGGGTTTGGCATCTGTGACAGATATCTGTGGAGGGGGCCCTTATTTACC 359
Qy 381 GGAAGCTTGTGTAATCCAGCGGTCTTACCAAGAAAGCCTGTGATGAAAAAAG 440
Db 360 GGAAGCTTGTGTAATCCAGCGGTCTTACCAAGAAAGCCTGTGATGAAAAAAG 419
Qy 441 AAGTTTGTATTTATTTATTTACTTTTGTGATTAATTAATTAATTTCTGTA 500
Db 420 AAGTTTGTATTTATTTATTTACTTTTGTGATTAATTAATTAATTTCTGTA 479
Qy 501 TTCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 525
Db 480 TTCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 504

RESULT 6
US-09-882-171-98

Sequence 98, Application US/09882171
Publication No. US20030175858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/047,600
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,615
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,597
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,502
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,633
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,583
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,617
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,618
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,503
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,592
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,581
PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,584
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,500
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,587
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,492
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,598
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,613
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,582
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,596
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,580
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,568
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,314
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,671
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,674
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,669
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,312
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,313
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,672
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,315
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/056,886
PRIOR FILING DATE: 1997-08-22
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PRIOR APPLICATION NUMBER: 60/056,908
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PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05

Query Match 91.1%; Score 486.6; DB 13; Length 504;
Best Local Similarity 99.0%; Pred. No. 5.2e-111;
Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 21 CCGAGCTGGCGAGAGTAGAGGAGGCGGTGCTCCGCGCGGTGGCGGTGCTATCGCT 80
DB 1 CCGAGCTGGCGAGAGTAGAGGAGGCGGTGCTCCGCGCGGTGGCGGTGCTATCGCT 59
QY 81 TCGCAGAACCTACTCAGCGACCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGT 140
DB 60 TCGCAGAACCTACTCAGCGACCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGT 119
QY 141 CTGCAAGCGGAGAGTAGAGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 200
DB 120 CTGCAAGCGGAGAGTAGAGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179
QY 201 TGAAGGCCACGTGAAGATGCTGCGGTGATATATCACTGATGATCAAGATAT 260
DB 180 TGAAGGCCACGTGAAGATGCTGCGGTGATATATCACTGATGATCAAGATAT 239
QY 261 TCATGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 320
DB 240 TCATGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
QY 321 GAGGGGTGTTGACATGTTGACACGAGATGCTGCTGCTGCGAGCGGGCCCTTATTTAC 380
DB 300 GAGGGGTGTTGACATGTTGACACGAGATGCTGCTGCTGCGAGCGGGCCCTTATTTAC 359
QY 381 GGAAGCTTGTGTCATATCCAGGCGTCTTACAGAAAAAGCTGTGATGAAAAAAG 440
DB 360 GGAAGCTTGTGTCATATCCAGGCGTCTTACAGAAAAAGCTGTGATGAAAAAAG 419
QY 441 AAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 500
DB 420 AAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 479
QY 501 TTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 525
DB 480 TTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 504

RESULT 7

US-09-809-391-252
Sequence 252, Application US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 252
LENGTH: 506
TYPE: DNA
ORGANISM: Homo sapiens
US-09-809-391-252

Query Match 89.6%; Score 478.6; DB 11; Length 506;
Best Local Similarity 97.4%; Pred. No. 5.1e-109;
Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 37 GTGAGGAGGCGGTGCTCCGCGCGGTGGCGGTGCTATCGCTTGGCAGAACTTACTCA 96
DB 2 GAGGATTTGGCAGGACCCSCCGCGGTGGCGGTGCTATCGCTTGGCAGAACTTACTCA 61

QY 97 GGCAGCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGCTGCTGCTGCAACGGGATGGA 156
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 QY 157 TAACGTGACGCCGAAATTAACATCCGCCCTTCTGCTTCACTGTGAAAGGCCACGTGAA 216
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 QY 217 GATGCTGGGCTGATATTAATCACTCACTGGTAAACAAGTATTCATGCTCATGTAATC 276
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 QY 277 TGTGTGGCACTGATATCAAGAAACCAACATGACAGTTGGTGAAGGGGTTGCACT 336
 Db 242 TGTGTGGCACTGATATCAAGAAACCAACATGACAGTTGGTGAAGGGGTTGCACT 301
 QY 337 TGTGACAGCATATCTCTTCTTCCGAGGGGCCCTTTATTAACCGAAGCTTCGTGCA 396
 Db 302 TGTGACAGCATATCTCTTCTTCCGAGGGGCCCTTTATTAACCGAAGCTTCGTGCA 361
 QY 397 TCCGAGCGCTCCTTACGAGAAAGCCTGTGCATGAAAAAGAGTTTGTATTTTA 456
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 QY 457 TATTACTTTTATGTTGATTAAGTAAATTAATTTCTGTATTTCTTCCAAAAAAA 516
 Db 422 TATTACTTTTATGTTGATTAAGTAAATTAATTTCTGTATTTCTTCCAAAAAAA 481
 QY 517 AAAAAAAAAAAAAA 533
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RESULT 8

US-09-882-171-252
 ; Sequence 252, Application US/09882171
 ; Publication No. US20030175858A1
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 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT APPLICATION NUMBER: US/09/882,171
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 09/809,391
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 09/149,476
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Query Match	89.6%;	Score 478.6;	DB 13;	Length 506;
Best Local Similarity	97.4%;	Pred. No. 5.1e-109;		
Matches 484;	Conservative 2;	Mismatches 11;	Indels 0;	Gaps 0;

QY	3	GTATGGGGAAGGGGGGAGTCTCGCCGCGGGTGGGAGTGTGGTATCGCTCCAGAACTTACTCA	96
Db	2	GCAGAGTTTGGCCAGAGACCCSCCGCGGTGGCGTTGGTATCGCTTCCAGAACTTACTCA	61
QY	97	GGGAGCCACTGAGAAAGTTGAGGGAAAGTCTGCTGCTGGGTCTGCAGACGATGGA	156
Db	62	GGGAGCCACTGAGAAAGTTGAGGGAAAGTCTGCTGCTGGGTCTGCAGACGATGGA	121
QY	157	TAACTGCAGCGGAAAAATAAAAATCATCGCCCTTCTGCTCAGTGTGAAAGGCGACGTAA	216
Db	122	TAACTGCAGCGGAAAAATAAAAATCATCGCCCTTCTGCTCAGTGTGAAAGGCGACGTAA	181
QY	217	GATGCTGGCGGTGGATTTATCACTCACTGGTAAACAAGATTTCATGCTCATCGTATC	276
Db	182	GATGCTGGCGGTGGATTTATTCATCTCACTGGTAAACAAGATTTCATGCTCATCGTATC	241
QY	277	TGTGTTGGACACTGATATACGAGAAACACAACAATTGACAGTTGGTGAAGGGGTTTGACACT	336
Db	242	TGTGTTGGACACTGATATACGAGAAACACAACAATTGACAGTTGGTGAAGGGGTTTGACACT	301
QY	337	TGTGACAGAGTATGCTGTCTTTCGCCAGCGGGCCCTTATTTTAAACGGAAAGCTTCTGTTCAA	396
Db	302	TGTGACAGAGTATGCTGTCTTTCGCCAGCGGGCCCTTATTTTAAACGGAAAGCTTCTGTTCAA	361
QY	397	TCCCAAGCGCTCTTACCGAGAAAAACCGTCGATGAAAAAAAAGAGTTTGGTAATTTTA	456
Db	362	TCCCAAGCGCTCTTACCGAGAAAAACCGTCGATGAAAAAAAAGAGTTTGGTAATTTTA	421
QY	457	TATTACTTTTATGTTGATATCAAGTATTTAAACATATTTCTGTAATCTTCCAAAAAAA	516
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QY	517	AAAAAAAAAAAAAAAAAAAA 533	
Db	482	AAAAAAAAAAAAAAAAAAAA 498	

RESULT 9
US-10-319-763-53
Sequence 53, Application US/10319763
Publication No. US2003014490A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Rouguerelet, Lydie
TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957

PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 53
LENGTH: 500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 197..288
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.5999990463257
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 464..469
FEATURE:
NAME/KEY: polyA_site
LOCATION: 489..500
FEATURE:
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LOCATION: 197..412
OTHER INFORMATION: homology
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 61..195
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LOCATION: 425..488
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LOCATION: 58..195
OTHER INFORMATION: homology

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Db 181 ACAACATTTGAAGTGTGTGAAGGGGTGTGTGCACTTGTGACAGAGTATGCTGTGCC 240
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Qy 422 CCTGTGATGAAAAAAGAGAGTTTGTAAATTTATTAATTTTGTGTGATGATAG 481
Db 301 CCGTGTGATGAAAAAAGAGTTTGTAAATTTATTAATTTTGTGTGATGATAG 360
Qy 482 TATTAAACATATTTCTGTATTTCTTCCAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 525
Db 361 TATTAAACATATTTCTGTATTTCTTCCAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 404

RESULT 14
US-10-242-535A-7940
Sequence 7940, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7940
LENGTH: 400
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (176)..(176)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-7940

Query Match 69.0%; Score 368.4; DB 12; Length 400;
Best Local Similarity 99.2%; Pred. No. 1,2e-81;
Matches 380; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 18 CCGCGCGGCGGCGGCTTCTATGCTTGCAGAACTTACTAGGACCCAGCTGAGAGA 77
Qy 115 GTTGAAGGAAGTCTGCTGTGCTGCAAGCGCATGATTAAGTCAAGCCGGAAT 174
Db 78 GTTGAAGGAAGTCTGCTGTGCTGCAAGCGCATGATTAAGTCAAGCCGGAAT 137
Qy 175 AAAACATGCGCCCTTCTGCTTCACTGTGAAGGCGAGTGAAGTCTGCGGCTGATAT 234
Db 138 AAAACATGCGCCCTTCTGCTTCACTGTGAAGGCGAGTGAAGTCTGCGGCTGATAT 197
Qy 235 TATCACTCACTGTGAACAAGATTTCAATGCTCATGCTGTGTGTCATGATACC 294

Db 198 TATCACTCACTGTGTGAACAAGATTTCAATGCTCATGCTGTGTGTCATGATACC 257
Qy 295 AGAACCACAACATTGACAGTTGTGTGAGGGGTGTGTGCA-CTTGTGACAGAGTATGCT 353
Db 258 AGAACCACAACATTGACAGTTGTGTGAGGGGTGTGTGCACTTGTGACAGAGTATGCT 317
Qy 354 GTCTTGGCGAGCGGGCCCTTATTATCCGGAAGCTTCTGTCAATCCAGCGGTCTTACC 413
Db 318 GTCTTGGCGAGCGGGCCCTTATTATCCGGAAGCTTCTGTCAATCCAGCGGTCTTACC 377
Qy 414 AGAAAAAGCCTGTGCATGAAAAA 436
Db 378 AGAAAAAGCCTGTGCATGAAAAA 400

RESULT 15
US-09-978-295A-189
Sequence 189, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Nadier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004

Query Match 62.7%; Score 335; DB 10; Length 663;

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2004, 03:35:03 ; Search time 1818 Seconds

(without alignments)
2227.752 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508
Sequence: 1 MDVNPQKIKRPFQCFYVKGH.....LFPNSGPYQKKPYHEKKEVL 99

Scoring table: BLOSUM62

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bites -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORES=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_hcg.*
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8: gb_pl.*
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13: gb_un.*
14: gb_vl.*
15: gb_da.*
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18: em_in.*
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35: em_htg_rdd.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	413	6 BD085952	BD085952 Elongatio
2	508	100.0	515	6 AR306550	AR306550 Sequence
3	508	100.0	515	6 AX061624	AX061624 Sequence
4	508	100.0	530	9 AF096895	AF096895 Homo sapi
5	491	96.7	526	6 AR275027	AR275027 Sequence
6	489	96.3	500	6 BD085905	BD085905 Elongatio
7	471.5	92.8	655	9 AF057306	AF057306 Homo sapi
8	471.5	92.8	669	6 AR306591	AR306591 Sequence
9	471.5	92.8	669	6 AX061665	AX061665 Sequence
10	471.5	92.8	688	9 BC004380	BC004380 Homo sapi
11	471.5	92.8	689	9 AF135380	AF135380 Homo sapi
12	461	90.7	415	6 BD023892	BD023892 Sequence
13	366	72.0	485	11 G30204	G30204 human STS S
14	339.5	66.8	593	6 AF145216	AF145216 Homo sapi
15	331	65.2	434	9 AF135381	AF135381 Homo sapi
16	323	63.6	321	6 BD139357	BD139357 Extended
17	318.5	62.7	495	6 AX079435	AX079435 Sequence
18	275	54.1	523	10 AF253064	AF253064 Rattus no
19	245	48.2	207	6 AX330610	AX330610 Sequence
20	245	48.2	207	6 AX330787	AX330787 Sequence
21	245	48.2	207	6 AX331008	AX331008 Sequence
22	245	48.2	207	6 AX408097	AX408097 Sequence
23	238.5	46.9	682	10 AF253065	AF253065 Rattus no
24	227.5	44.8	568	10 AY047360	AY047360 Mus muscu
25	215	42.3	151620	2 AC018589	AC018589 Homo sapi
26	215	42.3	180702	9 AC018557	AC018557 Homo sapi
27	215	42.3	188460	9 AC010542	AC010542 Homo sapi
28	198.5	39.1	682	10 AF401531	AF401531 Mus muscu
29	142	28.0	59554	9 AX695587	AX695587 Sequence
30	142	28.0	97075	9 AC010289	AC010289 Homo sapi
31	141.5	27.9	269	6 BD030595	BD030595 Sequence
32	139.5	27.5	527	10 AY046597	AY046597 Mus muscu
33	119	23.4	189981	2 AC137048	AC137048 Rattus no
34	119	23.4	209366	2 AC128918	AC128918 Rattus no
35	119	23.4	213593	2 AC131402	AC131402 Rattus no
36	119	23.4	249762	2 AC111422	AC111422 Rattus no
37	118	23.2	213593	2 AC131402	AC131402 Rattus no
38	118	23.2	273571	2 AC112851	AC112851 Rattus no
39	115	22.6	137334	10 AC121952	AC121952 Mus muscu
40	115	22.6	171595	2 AC121275	AC121275 Mus muscu
41	108	21.3	6283	6 AX252052	AX252052 Sequence
42	108	21.3	6283	6 AX344430	AX344430 Sequence
43	108	21.3	6283	6 AX346835	AX346835 Sequence
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RESULT 1

ALIGNMENTS

BD085952
LOCUS BD085952 413 bp DNA linear PAT 27-AUG-2002
DEFINITION Elongation cDNA of secretory protein.
ACCESSION BD085952
VERSION BD085952.1 GI:22631562
KEYWORDS JP 2001523453-A/94.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bougueleret, L., Duclert, A. and Edwards, J.B.D.M.
TITLE Elongation cDNA of secretory protein
JOURNAL Patent: JP 2001523453-A 94 27-NOV-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001523453-A/94
PD 27-NOV-2001
PR 13-NOV-1998 JP 2000521191
PR 13-NOV-1997 US 60/066677,17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121,13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PI
BOUGUELERET, AYMERIC DUCLERT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
Von Heijne matrix
CC score 4.09999990463257
CC seq VFMLIVSVLALIP/ET
FH key Location/Qualifiers
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BASE COUNT 121 a 82 c 95 g 115 t

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Score: 508.00 Matches: 99
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

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QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 106 GTGAAGATGCGCGCGGTGATATTAATCACTGGAACAACAGATTTCATCTCATC 165
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 166 GTATCTGTGGTGGACATGATACCGAAGAACCAACATTTGACAGTTGGTGGAGGGGCTTTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 226 GCACCTTGTGACGAGATGCTGCTTGGCGAGCGGGCCCTTATTACCGAGAGCTTCTG 285
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGluLysGlyValLeu 99
DB 286 TTCAATCCACGCGCTCTTACCAAGAAAAGCCTGTGCATGAAAAAAGAAAGTTTGG 342

RESULT 2
AR306550
AR306550

LOCUS AR306550 515 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 29 from patent US 6548633.
ACCESSION AR306550
VERSION AR306550.1 GI:31696619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 515)
TITLE Edwards, J.-B.D.M., Bougueleret, L. and Jobert, S.
JOURNAL Complementary DNA's encoding proteins with signal peptides
PATENT: US 6548633-A 29 15-APR-2003;
FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 3.88e-56 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB 144 ATGATTAACGTGGCGCGGAAATTAACATCGCCCTTCGCTTCAGTGAAGGCGCAC 203
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 204 GTGAAGATGCGCGCGGTGATATTAATCACTGGAACAACAGATTTCATCTCATC 263
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 264 GTATCTGTGGTGGACATGATACCGAAGAACCAACATTTGACAGTTGGTGGAGGGGCTTTT 323
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 324 GCACCTTGTGACGAGATGCTGCTTGGCGAGCGGGCCCTTATTACCGAGAGCTTCTG 383
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGluLysGlyValLeu 99
DB 384 TTCAATCCACGCGCTCTTACCAAGAAAAGCCTGTGCATGAAAAAAGAAAGTTTGG 440

RESULT 3
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Sequence 29 from Patent WO0100806.
ACCESSION AX061624
VERSION AX061624.1 GI:12406709
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
PATENT: WO 0100806-A 29 04-JAN-2001;
GENSET (FR)

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/protein_id="CAC24985.1"

CDS

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144 . .287
/notes="Von Heijne matrix score 4.10 seq VFMILVSVLALIR/ET"
polya_signal 457 . .462
polya_site 500 . .515
BASE COUNT 143 a 106 c 135 g 130 t 1 others
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Alignment Scores:
Pred. No.: 3.88e-56 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-801-115B-2 (1-99) x AX061624 (1-515)
QY 1 MetAspAsnValGlnProLysIleLeuHisArgProPheCysPheSerValLysGlyHis 20
Db 144 ATGATTAAGTGTGACGAGCGGAAATTAACATCGCCCTTCTGCTTCACTGGAAGGCCAC 203
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 204 GTGAAGATGCTGCGGCTGGATTAATTAATCACTGCTGTAACAACAGATTCAATGCTCATC 263
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 264 GATCTGTGTGGACATGATACCAAGAAACCAACATTTGACATGATGGAGGGGCTTTT 323
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleArgLysLeuLeu 80
Db 324 GCACCTGTGACAGCAGATGCTGTCTTCCGACGGGCGCTTATTTTCCGAAAGCTTCTG 383
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGluLysGlyValLeu 99
Db 384 TTCATCCCGCGGCTCTTCCGAAAGCGCTGTGATGATGAAAAAGAGTTTGG 440
RESULT 4
AF096895 530 bp mRNA linear PRI 18-JUN-2001
LOCUS Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.
DEFINITION AF096895
ACCESSION AF096895.2 GI:9989691
VERSION FL1_CDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 530)
Han,W., Lou,Y., Tang,J., Zhang,Y., Chen,Y., Li,Y., Gu,W., Huang,J.,
Gul,L., Tang,X., Li,F., Song,Q., Di,C., Wang,L., Shi,Q., Sun,R.,
Xia,D., Rui,M., Tang,J. and Ma,D.
Molecular cloning and characterization of chemokine-like factor 1
(CKLF1), a novel human cytokine with unique structure and potential
chemotactic activity
Biochem. J. 357 (Pt 1), 127-135 (2001)
JOURNAL MEDLINE 21308461
PUBMED 11415443
REFERENCE 2 (bases 1 to 530)
AUTHORS Han,W.L., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38
Xue Yuan Rd., Beijing 100083, China
3 (bases 1 to 530)
Han,W.L.
Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK Sequence update by submitter
COMMENT On Sep 7, 2000 this sequence version replaced gi:6288733.
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FEATURES
source
Location/Qualifiers
1..530
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/notes="exposed to phytohaemagglutinin (PHA)"
1..530
/gene="CKLF1"
/notes="synonym: UCK-1"
148..447
/gene="CKLF1"
/notes="increased expression in PHA stimulated cells;
expression inhibited by IL-10"
/codon_start=1
/product="chemokine-like factor 1"
/protein_id="AA06732.1"
/db_xref="GI:6288734"
/translation="MDNVQPKIKRPFCSVKGHVZMLRDIINSLVTVFMILVSVL
ALIPETTLTVGGVFLVAVCCADGALIVRKLFPNSGPYQKRVHEKKEVL"
BASE COUNT 156 a 108 c 137 g 129 t
ORIGIN
Alignment Scores:
Pred. No.: 4.02e-56 Length: 530
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-801-115B-2 (1-99) x AF096895 (1-530)
QY 1 MetAspAsnValGlnProLysIleLeuHisArgProPheCysPheSerValLysGlyHis 20
Db 148 ATGATTAAGTGTGACGAGCGGAAATTAACATCGCCCTTCTGCTTCACTGGAAGGCCAC 207
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 208 GTGAAGATGCTGCGGCTGGATTAATTAATCACTGCTGTAACAACAGATTCAATGCTCATC 267
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 268 GATCTGTGTGGACATGATACCAAGAAACCAACATTTGACATGATGGAGGGGCTTTT 327
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleArgLysLeuLeu 80
Db 328 GCACCTGTGACAGCAGATGCTGTCTTCCGACGGGCGCTTATTTTCCGAAAGCTTCTG 387
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGluLysGlyValLeu 99
Db 388 TTCATCCCGCGGCTCTTCCGAAAGCGCTGTGATGATGAAAAAGAGTTTGG 444
RESULT 5
AR275027 526 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 164 from patent US 6506607.
DEFINITION AR275027
ACCESSION AR275027.1 GI:29707577
VERSION AR275027.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 526)
AUTHORS Shyjan,A.W.
TITLE Methods and compositions for the identification and assessment of
prostate cancer therapies and the diagnosis of prostate cancer
Patent: US 6506607-A 164 14-JAN-2003;
JOURNAL Location/Qualifiers
FEATURES
source
1..526
/organism="unknown"
BASE COUNT 133 a 136 c 113 g 143 t 1 others
ORIGIN
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source 1. .500
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 135 a 102 c 125 g 129 t 9 others

ORIGIN

Alignment Scores:
Pred. No.: 1.05e-53 Length: 500
Score: 489.00 Matches: 98
Percent Similarity: 98.00% Conservative: 0
Best Local Similarity: 98.00% Mismatches: 1
Query Match: 96.26% Indels: 1
Gaps: 0

US-09-801-115b-2 (1-99) x BD085905 (1-500)

QY 1 MetAspAsnValGlnProLysIleYshHlaArgProPheCysPheSerValIyGlyHis 20
|||
Db 132 ATGGATTAACGTGACGCGGAAATAAACATCGCCCTTCGCTTCAGTGGAAAGGCCAC 191
|||
QY 21 ValMetLeuArgLeuAspIleLeuSerLeuValThrThrValPheMetLeu1 40
|||
Db 192 GTGAGATGCTGGCTGGATTAATCACTCACTGTAACACAGATTCATGCTCAT 251
|||
QY 40 eValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAla 60
|||
Db 252 CGTATCTGTGGCATGATGATACAGAAACACACATTCAGATTCGTGGAGGGGTGT 311
|||
QY 60 eAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
|||
Db 312 TGCACTGTGACAGCAGATATGCTGTGGCGAGCGGGCCCTTATTAACCGGAAGCTTCT 371
|||
QY 80 uPheAsnProSerGlyProTyrGlnLysLysProValHisGlnLysGluValLeu 99
|||
Db 372 GTTCAATCCAGCGGCTCTTACCGAAAGAGCTGTGATGAAAGAGAGTTTG 429
|||

RESULT 7
AF057306 655 bp mRNA linear PRI 31-DEC-1999
LOCUS AF057306
DEFINITION Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.
ACCESSION AF057306
VERSION AF057306.1 GI:6648618
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 655)
REFERENCE Zhang,J.S., Nelson,M., Wang,L. and Smith D.I.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic
and Foundation, Rochester, MN 55905, USA
location/Qualifiers
1. .655
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="AsPC-1"
/tissue_type="pancreas"
/note="adenocarcinoma"
1. .655
/gene="C32"
132. .590
/gene="C32"
/note="down regulated upon cell differentiation induced by
sodium butyrate"
/codon_start=1
/product="transmembrane proteolipid"
/protein_id="AAF2125.1"
/db_xref="GI:6648619"
/translation="MDNVQPKIKRPFQSVKGVKMLRLALVTSTMTFFLIQAQPP
YVITGEVTVILFFILLYRLDLRLMKMLFPLDIINSIVTTFMLIVSVALIBE

gene
CDS

TTTITVGGVFAVLTAVCCLAGALTYRKLIFNPSPGYOKKPYHEKEVYL"

BASE COUNT 171 a 137 c 153 g 194 t

ORIGIN

Alignment Scores:
Pred. No.: 2.66e-51 Length: 655
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
Gaps: 1

US-09-801-115b-2 (1-99) x AF057306 (1-655)

QY 1 MetAspAsnValGlnProLysIleYshHlaArgProPheCysPheSerValIyGlyHis 20
|||
Db 132 ATGGATTAACGTGACGCGGAAATAAACATCGCCCTTCGCTTCAGTGGAAAGGCCAC 191
|||
QY 21 ValMetLeuArg----- 25
|||
Db 192 GTGAGATGCTGGCTGGATTAATCACTCACTGTAACACAGATTCATGCTTTTATCATGCACAA 251
|||
QY 25 ----- 25
|||
Db 252 GCCCTGACCAATATATTGTATCACTGATTTGAAGTCAACCGTTATCTTATTTTCATA 311
|||
QY 26 -----LeuAsp 27
|||
Db 312 CTTTATATGATCTACAGCTTGATCGATTATGAAGTGTATTGCGCTTGCTTGAT 371
|||
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
|||
Db 372 ATTATCACTCACTGATGTAACACAGATTCATGCTCATCTGATCTGTGGACATGATA 431
|||
QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
|||
Db 432 CCAAAACCAACACATTGACAGATTTGGAGGGGTGTTTCACCTTGACAGCAGATATGC 491
|||
QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87
|||
Db 492 TGCTTCCCGACGCGGCTTATTTACCGAAGCTTCTGTCAATCCACGCGGTCTTAC 551
|||
QY 88 GlnLysLysProValHisGlnLysGluValLeu 99
|||
Db 552 CAGAAAGAGCTGTGATGAAAGAGAGTTTG 587
|||

RESULT 8
AR306591 669 bp DNA linear PAT 12-JUN-2003
LOCUS AR306591
DEFINITION Sequence 70 from patent US 6548633.
ACCESSION AR306591
VERSION AR306591.1 GI:31696660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 669)
AUTHORS Edwards,J., B.D.M., Bougueleret,L. and Jobert,S.
TITLE Complementary DNA's encoding proteins with signal peptides
JOURNAL Patent: US 6548633-A 70 15-APR-2003;
location/Qualifiers
1. .669
/organism="unknown"
BASE COUNT 178 a 139 c 158 g 194 t

ORIGIN

Alignment Scores:
Pred. No.: 2.73e-51 Length: 669
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
Gaps: 1

US-09-801-115B-2 (1-99) x AR306591 (1-669)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 140 ATGGATACCTGCAGCGGAAATAAACATCGCCCTTGTGCTTCAAGTGAAGGCGCAC 199

QY 21 ValLysMetLeuArg----- 25
Db 200 GTGAAGATGCTGGCGCTGGCAGCTACTGTGACATCTATGACCTTTTATCATGCACAA 259

QY 25 ----- 25
Db 260 GCCCGTGAACCATATATTGTTATCATCTGATTGAAGTACCGTTATCTTATTTTCATA 319

QY 26 -----LeuAsp 27
Db 320 CTTTATATGACTCAGACTTGATCGATTAAATGAAGGTATTATTTGGCCTTGTGAT 379

QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
Db 380 ATTATCACTCACTGCTGTACACAGATATTCTCATCTCATCTGCTGTGGCAGTATA 439

QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 440 CCAGAAACCAACAATTGACAGTGTGGAGGGGTGTTCACCTTGATCGACAGCATATGC 499

QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuPheAsnProSerGlyProTyr 87
Db 500 TGTCTTCCAGCGGGCCCTTATTATTCAGGAAGCTTGTGTCAATCCAGCGGTCTTAC 559

QY 88 GlnLysLysProValHisGluLysLysGluValLeu 99
Db 560 CAGAAAAAGCCTGTGCATGAATAAAAAAGAACTTTTG 595

RESULT 9
LOCUS AX061665 669 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 70 from Patent WO0100806.
ACCESSION AX061665
VERSION AX061665.1 GI:12406789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 dumas mine Edwards, J.B., Bouguetelaret, I. and Jobert, S.
AUTHORS Complementary dna's encoding proteins with signal peptides
TITLE Patent: WO 0100806-A 70 04-JAN-2001;
JOURNAL GENSET (FR)

FEATURES
Location/Qualifiers
1..669
/organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
140..598
/note="unamed protein product"
/codon start=1
/protein id="CAC25025.1"
/db xref="GI:12406790"
/translation="MDNVOPKIKRPFCESVKGVKMLRLATVTSMTFFIIQAAPP
YIVTGTGPEVYILFFILLXVLRIDRLMKMLFPLDITINSIVTVMILVSLALIBE
TTTLVGGGVAVLTAVCCLDGALIRKLFPNSGPRKPRVHEKEVLT"

CDS
140..442
/note="Von Heijne matrix score 4.10 seq VFMLIVSLALIP/ET"
polyA signal
630..635
polyA site 655..669
BASE COUNT 178 a 139 c 158 g 194 t
ORIGIN

Alignment Scores:
Pred. No.: 2.73e-51 Length: 669

Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 53
Query Match: 92.81% Indels: 1
DB: 6 Gaps: 1

US-09-801-115B-2 (1-99) x AX061665 (1-669)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 140 ATGGATACCTGCAGCGGAAATAAACATCGCCCTTGTGCTTCAAGTGAAGGCGCAC 199

QY 21 ValLysMetLeuArg----- 25
Db 200 GTGAAGATGCTGGCGCTGGCAGCTACTGTGACATCTATGACCTTTTATCATGCACAA 259

QY 25 ----- 25
Db 260 GCCCGTGAACCATATATTGTTATCATCTGATTGAAGTACCGTTATCTTATTTTCATA 319

QY 26 -----LeuAsp 27
Db 320 CTTTATATGACTCAGACTTGATCGATTAAATGAAGGTATTATTTGGCCTTGTGAT 379

QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
Db 380 ATTATCACTCACTGCTGTACACAGATATTCTCATCTCATCTGCTGTGGCAGTATA 439

QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 440 CCAGAAACCAACAATTGACAGTGTGGAGGGGTGTTCACCTTGATCGACAGCATATGC 499

QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuPheAsnProSerGlyProTyr 87
Db 500 TGTCTTCCAGCGGGCCCTTATTATTCAGGAAGCTTGTGTCAATCCAGCGGTCTTAC 559

QY 88 GlnLysLysProValHisGluLysLysGluValLeu 99
Db 560 CAGAAAAAGCCTGTGCATGAATAAAAAAGAACTTTTG 595

RESULT 10
LOCUS BC004380 688 bp mRNA linear PRI 12-JUN-2001
DEFINITION Homo sapiens, clone MGC:10658 IMAGE:3639550, mRNA, complete cds.
ACCESSION BC004380
VERSION BC004380.1 GI:13325133
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 688)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Buterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garfield, Ran Guo,
Leticia Hsiao, Martin Krzywnski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Scott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAL Plate: 13 Row: f Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9989692.
Location/Qualifiers

FEATURES

source

1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:10658 IMAGE:3639550"
/tissue_type="Pancreas, adenocarcinoma"
/clone_id="NIH MGC 39"
/lab_host="DH10B-R"
/note="Vector: pOT87"
137..595
/codon_start=1
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/protein_id="AAH04380.1"
/db_xref="GI:13325134"
/translation="MDNVQPKIRHRCPCSVKGVKMLRLALVTSTMTPTIIAQP
YVITGEBTVILFLLVLRDRLMKLFWPLDIINSLVTVFMILVSLALIE
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CDS

BASE COUNT 201 a 138 c 154 g 195 t
ORIGIN

Alignment Scores:

Pred. No.: 2.82e-51 Length: 688
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x BC004380 (1-688)

QY 1 MetAspAsnValGlnProIysIleIysHISARgProhCysPheSerValIysGlyHis 20
DB 137 ATGGATACGTGACGCCGAAATTAACATCGCCCTTCCTTCAGTGGAAAGGCCAC 196
QY 21 ValIysMetLeuArg----- 25
DB 197 GTGAAGATGCTGGCGGCTGGCACTAGTGCATCTATGACCTTTTATCATCGCACAA 256
QY 25 ----- 25
DB 257 GCCCGTGAACATATATTGTTATCATGATTGAAGTCAACCGTTATCTTATTTTCATA 316
QY 26 -----LeuAsp 27
DB 317 CTTTATATGACTACAGACTTGATCGATTATGAAGAGGTTATTTGGCCTTGCTTGAT 376
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47
DB 377 ATTATCACTCACTGCTGTAACAACAGTATTCATGCTCATCTGATCTGTTGGCACTGATA 436
QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
DB 437 CCGAAACCAACAACATTTGACAGTTGGTGGAGGGGTGTTTGCACTTGAGACGAGTATGC 496
QY 68 CysLeuAlaAspGlyAlaLeuIleIleIleIleIleIleIleIleIleIleIleIleIle 87
DB 497 TGTCTTCCGACGGGGCCCTTATTTACCGGAAGCTTCCTGTTCAATCCAGGAGTCTTAC 556
QY 88 GlnIysLysProValHisGluIysLysGluValLeu 99
DB 557 CAGAAAAGCCTGTGCATGAAAAAAGAGATTG 592
RESULT 11
AF135380

LOCUS AF135380 689 bp mRNA linear PRI 07-SEP-2000
DEFINITION Homo sapiens chemokine-like factor 2 (CXCLF2) mRNA, complete cds,
alternatively spliced.
ACCESSION AF135380
VERSION AF135380.2 GI:9989692
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

1 (bases 1 to 689)
Han, W.L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.
Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
2 (bases 1 to 689)
Han, W.L.
Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:6630853.
Location/Qualifiers

FEATURES

source

gene

CDS

1..689
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1..689
/gene="CXCLF2"
/note="CXCLF2"
148..606
/gene="CXCLF2"
/note="CXCLF2"
/note="Uck-2, alternatively spliced"
/codon_start=1
/product="chemokine-like factor 2"
/protein_id="AF19599.1"
/db_xref="GI:6630854"
/translation="MDNVQPKIRHRCPCSVKGVKMLRLALVTSTMTPTIIAQP
YVITGEBTVILFLLVLRDRLMKLFWPLDIINSLVTVFMILVSLALIE
TTTLVGGVFAVLTAVCCADGALIRKLLFNPSGPYQKKPVHEKKEVL"

BASE COUNT 195 a 140 c 161 g 193 t
ORIGIN

Alignment Scores:

Pred. No.: 2.83e-51 Length: 689
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF135380 (1-689)

QY 1 MetAspAsnValGlnProIysIleIysHISARgProhCysPheSerValIysGlyHis 20
DB 148 ATGGATACGTGACGCCGAAATTAACATCGCCCTTCCTTCAGTGGAAAGGCCAC 207
QY 21 ValIysMetLeuArg----- 25
DB 208 GTGAAGATGCTGGCGGCTGGCACTAGTGCATCTATGACCTTTTATCATCGCACAA 267
QY 25 ----- 25
DB 268 GCCCGTGAACATATATTGTTATCATGATTGAAGTCAACCGTTATCTTATTTTCATA 327
QY 26 -----LeuAsp 27
DB 328 CTTTATATGACTACAGACTTGATCGATTATGAAGGTTATTTGGCCTTGCTTGAT 387
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47

Db 388 ATTATCACTCATCTGTAACAACAGATATTCATCTGATCTGTGTGGCAGCTGATA 447
Qy 48 ProgluThrThrThrThrThrThrThrValGlyGlyValPheAlaLeuAlaThrAlaValCys 67
Db 448 CCAAGAACCAACAACATTACAGCTTGAGAGGGGTTTGGCATTGGACAGCAGTATGC 507
Qy 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuPheAsnProSerGlyProTyr 87
Db 508 TGTCTGCGACGGGGGCTTATTATTCACCGAAGCTTCTTCATCCAGCGGTCCTTAC 567
Qy 88 GlnLysLysProValHisGlnLysGlnValLeu 99
Db 568 CAGAAAAAGCCTGTGCATGAAAAAAGAGTTTGG 603

RESULT 12
BD023892 415 bp DNA linear PAT 27-AUG-2002
LOCUS Sequence tag and encoded human protein.
DEFINITION BD023892
ACCESSION BD023892.1 GI:22565115
VERSION JP 2001269182-A/138.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 138 02-OCT-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/138
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC score 4.1
CC seq VFWLIVSVLALIP/ET
FH Key Location/Qualifiers
FT CDS 146..415
FT sig_peptide 146..289.
FT Location/Qualifiers
1..415
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 101 a 97 c 126 g 91 t

ORIGIN

Alignment Scores:
Pred. No.: 3,41e-50 Length: 415
Score: 461.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.75% Indels: 0
DB: 6 Gaps: 0

US-09-801-115B-2 (1-99) x BD023892 (1-415)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 146 ATGGATAACGTGCAGCCGAAATATAAATACATCGCCCTCTCTCCTCAGGTGAAAGGCAC 205
Qy 21 ValLysMetLeuAlaGluAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 206 GTGAGAGATGCTGGCTGTGATATTAATCAATCAGTGTAAACAGATATTATCTCATC 265
Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

Db 266 GATCTGTGTGGCAGCTGATACAGAAACCAACAACATTGACAGTTGTGAGGGGTTT 325
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
Db 326 GCAGCTGTGACACAGATATCTGTCTTGGACGGGGGCTTATTATTCAGGAAGCTTCTG 385
Qy 81 PheAsnProSerGlyProTyrGlnLys 90
Db 386 TTCATCCAGCGGCTCTTACAGAAAAAG 415

RESULT 13
G30204 485 bp DNA linear STS 05-OCT-1996
LOCUS human STS SHGC-36487, sequence tagged site.
DEFINITION G30204
ACCESSION G30204
VERSION G30204.1 GI:1593755
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE STS; STS sequence (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, W-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: ACTTCTTTTTCATGCACAGC
Primer B: GCCCTATTACGGAGCT
STS size: 77
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90569
-- Washington University/Merck EST sequence.
Location/Qualifiers
1..485
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="16"
69..145
69..91
STS primer_bind complement(126..145)
BASE COUNT 146 a 99 c 99 g 131 t 10 others
ORIGIN

Alignment Scores:

Pred. No.: 7.32e-38 Length: 485
Score: 366.00 Matches: 73
Percent Similarity: 98.65% Conservative: 0
Best Local Similarity: 98.65% Mismatches: 1
Query Match: 72.05% Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x G30204 (1-485)

QY 26 LeuAspIleIleAsnSerLeuValThrThValPheMetLeuIleValSerValIleuAla 45
Db 286 CTGATATTTCACCTACCTGCTGACACAGTATTCATGCTCATCGAATCGTGGCA 227
QY 46 LeuIleProGluThrThrThrIleuThrValGlyGlyValPheAlaIleuValThrAla 65
Db 226 CTGATACCAAGAACACACACATTGACAGTGTGAGAGGGGTGTGGACCTTGACAGCA 167
QY 66 ValCysCysLeuAlaAspGlyValAlaLeuIleTyThrArgLysLeuLeuPheAsnProSerGly 85
Db 166 GTATGCTGTCTTCCGACGGGGCCCTTATTACCGAGAGCTTCTGTCATCCACGGGT 107
QY 86 ProTyArgLysLysProValHisGluLysGluValLeu 99
Db 106 CTTTACCAGAAAAGCTGTGCAATGAAAAAGAAAGTTTG 65

RESULT 14

AF145216 593 bp mRNA linear PRI 07-SEP-2000
LOCUS Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF145216
VERSION AF145216.2 GI:9989694
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 593)
Han, W.L., Gu, W.F., Li, Y., Zhang, Y.M., Di, C.H., Song, Q.S. and
Ma, D.L.

TITLE Direct Submission
JOURNAL Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
REFERENCE
AUTHORS 2 (bases 1 to 593)
Han, W.L.

JOURNAL Direct Submission
REMARK Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
COMMENT Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:625671.

FEATURES

source
1..593
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1..593
/gene="CKLF4"
/note="synonym: UCK"
148..510
/gene="CKLF4"
/note="UCK-4; alternatively spliced"
/codon_start=1
/product="chemokine-like factor 4"
/protein_id="AAFI9350.1"
/db_xref="GI:625672"
/translation="MDNVQPKIRBPFCFSVKGHVKKRLATLTVTSMTFFIIAQPAP
YVITGTEVTVIIFLILYVLRDRMLKMLFWPLVAVATVAVCCADGALIIYKLLF
NBSGPYKKEVHEKEVTL"

BASE COUNT 166 a 120 c 140 g 167 t
ORIGIN

Alignment Scores:
Pred. No.: 2.45e-34 Length: 593
Score: 339.50 Matches: 73
Percent Similarity: 61.90% Conservative: 5
Best Local Similarity: 57.94% Mismatches: 15
Query Match: 66.83% Indels: 33
DB: 9 Gaps: 2

US-09-801-115B-2 (1-99) x AF145216 (1-593)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 148 ATGGATACGTCGACGAGCGAAATATAACATCGCCCTTCTGCTTCATGTAAGGCCAC 207
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 208 GTGAAGATCTGTGGCTGGACACTA-----ACTGTGACATCATGACC 249
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGly----- 58
Db 250 TTTTATCATGACACAGCCCTGAAACCATATATTTATCATCTGATTTGAAGTCACC 309
QY 58 ----- 58
Db 310 GTTATCTTATTTTCTCACTTATATGATGATGACACTGATGATTAATGAAGTGTTA 369
QY 59 -----ValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAla 73
Db 370 TTTTGCCCTTGTGCTGTGTTTGACCTTGACAGCAGTATGCTGTTCGCCAGGGGCC 429
QY 74 LeuIleTyArgLysLeuLeuPheAsnProSerGlyProTyArgLysLysProValHis 93
Db 430 CTTATTTACCGAGAGCTTCTGTCATCCACAGCGCTCTTACAGAAAAAGCCTGTGCAI 489
QY 94 GluLysGluValLeu 99
Db 490 GAAAAAAGAAAGTTTG 507

RESULT 15

AF135381 434 bp mRNA linear PRI 07-SEP-2000
LOCUS Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF135381
VERSION AF135381.2 GI:9989693
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 434)
Han, W.L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.

TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
REFERENCE
AUTHORS 2 (bases 1 to 434)
Han, W.L.

JOURNAL Direct Submission
REMARK Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
COMMENT Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:6630855.

FEATURES

source
1..434
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1..434
/gene="CKLF3"
/note="UCK"
148..351

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/gene="CKLF3"
/note="UCK-3: alternatively spliced"
/codon_start=1
/product="chemokine-like factor 3"
/protein_id="AF19600.1"
/db_xref="GI:6630856"
/translation="MDNVOPKIKRPFCSYKGVKMLRLVFAVLTAVCCILADGALIY
RKLFNPSGYPQKKVHEKKEVL"

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BASE COUNT 127 a 88 c 116 g 103 t
ORIGIN

Alignment Scores:

Pred. No.:	2.08e-33	Length:	434
Score:	331.00	Matches:	67
Percent Similarity:	67.68%	Conservative:	0
Best Local Similarity:	67.68%	Mismatches:	0
Query Match:	65.16%	Indels:	32
DB:	9	Gaps:	1

US-09-801-115b-2 (1-99) x AF135381 (1-434)

QY	1	MetAspAsnValGlnProLysIleLeuHisArgProPheCysPheSerValLysGlyHis	20
Db	148	ATGGATACGTCAGCCGAAATAAATACATGCCCCCTTCTCAGTGTAAGGCCAC	207
QY	21	ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle	40
Db	208	GTGAAGATGCTGCGGCTG-----	225
QY	41	ValSerValLeuAlaLeuIleProGlnThrThrThrLeuThrValGlyGlyValPhe	60
Db	226	-----GTGTTT	231
QY	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu	80
Db	232	GCACTTGACAGCAGTATGCTGCTTGCACGCGGCGCTTATTTACCGAAGCTTCTG	291
QY	81	PheAsnProSerGlyProTyrGlnLysLysProValHisGlnLysGluValLeu	99
Db	292	TTCAATCCACGGGTCCTTACAGAAAGAGCTGTGATGAAAGAAAGAGTTTG	348

Search completed: January 31, 2004, 04:50:56
Job time : 1820 secs

NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 147
LENGTH: 413
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 46..189
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.0999990463257
OTHER INFORMATION: seq VFMLIVSLALIP/ET
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 377..382
FEATURE:
NAME/KEY: polyA_site
LOCATION: 402..413
US-10-319-763-147

Alignment Scores:
Pred. No.: 4,97e-64 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-801-115B-2 (1-99) x US-10-319-763-147 (1-413)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20
DB 46 ATGATTAACGTGCAGCGCAAAATAAACATCGCCCTTCTCTCAGTGTAAAGCCAC 105
QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 106 GTGAGATGCTGCGCGCTGGAATATTAACAACCTGCTGTAACAACAAGATTCATCTATC 165
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 166 GTACTGTGTGGCATCATATCCAGAAACCAACATTGACATGGTGGAGGGGTGTTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArgLysLeu 80
DB 226 GCACCTGTGACAGCATATGCTGCTGCGACGCGGCGCTTATTATCCGGAACCTTCTG 285
QY 81 PheAsnProSerGlyProTyrrGlnLysPheProValHisGluLysGluValLeu 99
DB 286 TTCAATCCACGCGGTCTTACCAAGAAAGCGCTGTGATGAAAAAGAAAGTTTGG 342

RESULT 2

US-09-918-995-6534
Sequence 6534, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6534
LENGTH: 422
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-6534
Alignment Scores:
Pred. No.: 5.13e-64 Length: 422

Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-918-995-6534 (1-422)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20
DB 31 ATGATTAACGTGCAGCGCAAAATAAACATCGCCCTTCTCTCAGTGTAAAGCCAC 90
QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 91 GTGAGATGCTGCGCGCTGGAATATTAACAACCTGCTGTAACAACAAGATTCATCTATC 150
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 151 GTACTGTGTGGCATCATATCCAGAAACCAACATTGACATGGTGGAGGGGTGTTT 210
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArgLysLeu 80
DB 211 GCACCTGTGACAGCATATGCTGCTGCGACGCGGCGCTTATTATCCGGAACCTTCTG 270
QY 81 PheAsnProSerGlyProTyrrGlnLysPheProValHisGluLysGluValLeu 99
DB 271 TTCAATCCACGCGGTCTTACCAAGAAAGCGCTGTGATGAAAAAGAAAGTTTGG 327

RESULT 3

US-09-822-846-397
Sequence 397, Application US/09822846
Publication No. US2003027139A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechel, Kim
APPLICANT: Homes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakkar
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 397
LENGTH: 439
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-846-397
Alignment Scores:
Pred. No.: 5.44e-64 Length: 439
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-822-846-397 (1-439)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIlySGlyHis 20
Db 81 ATGGATACCTGACGACCGAATAAATCAATCGCCCTTCTGCTTCACTGAGAAAGCCAC 140

Qy 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 141 GTGAAGATGCTGGCGGATATATATCACTGATCACTGGTAAACAAGATTATCATGCTCATC 200

Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 201 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTGTGTGAGGGGTGTTT 260

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyValaLeuIleTyrrArgLysLeu 80
Db 261 GCACCTGTGACAGAGATGATCTGTCTTCCGACGGGCGCCCTTATTTACCGAAAGCTTCTG 320

Qy 81 PheAsnProSerGlyProTyrrGlnLysLysProValHisGlnLysGlyValLeu 99
Db 321 TTCAATCCAGCGGTCTCTTACGAAAGCCTGTGATATAAAGAAAGATTGTTG 377

RESULT 4

US-09-809-391-98
; Sequence 98, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-98

Alignment Scores:

Pred. No.:	6,68e-64	Length:	504
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-809-391-98 (1-504)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIlySGlyHis 20
Db 131 ATGGATACCTGACGACCGAATAAATCAATCGCCCTTCTGCTTCACTGAGAAAGCCAC 150

Qy 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 191 GTGAAGATGCTGGCGGATATATATCACTGATCACTGGTAAACAAGATTATCATGCTCATC 250

Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 251 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTGTGTGAGGGGTGTTT 310

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyValaLeuIleTyrrArgLysLeu 80
Db 311 GCACCTGTGACAGAGATGATCTGTCTTCCGACGGGCGCCCTTATTTACCGAAAGCTTCTG 370

Qy 81 PheAsnProSerGlyProTyrrGlnLysLysProValHisGlnLysGlyValLeu 99
Db 371 TTCAATCCAGCGGTCTCTTACGAAAGCCTGTGATATAAAGAAAGATTGTTG 427

RESULT 5

US-09-882-171-98
; Sequence 98, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-882-171-98

US-09-801-115B-2 (1-99) x US-09-822-846-397 (1-439)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIlySGlyHis 20
Db 81 ATGGATACCTGACGACCGAATAAATCAATCGCCCTTCTGCTTCACTGAGAAAGCCAC 140

Qy 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 141 GTGAAGATGCTGGCGGATATATATCACTGATCACTGGTAAACAAGATTATCATGCTCATC 200

Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 201 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTGTGTGAGGGGTGTTT 260

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyValaLeuIleTyrrArgLysLeu 80
Db 261 GCACCTGTGACAGAGATGATCTGTCTTCCGACGGGCGCCCTTATTTACCGAAAGCTTCTG 320

Qy 81 PheAsnProSerGlyProTyrrGlnLysLysProValHisGlnLysGlyValLeu 99
Db 321 TTCAATCCAGCGGTCTCTTACGAAAGCCTGTGATATAAAGAAAGATTGTTG 377

RESULT 4

US-09-809-391-98
; Sequence 98, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-98

Alignment Scores:

Pred. No.:	6,68e-64	Length:	504
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-809-391-98 (1-504)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIlySGlyHis 20
Db 131 ATGGATACCTGACGACCGAATAAATCAATCGCCCTTCTGCTTCACTGAGAAAGCCAC 150

Qy 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 191 GTGAAGATGCTGGCGGATATATATCACTGATCACTGGTAAACAAGATTATCATGCTCATC 250

Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 251 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTGTGTGAGGGGTGTTT 310

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyValaLeuIleTyrrArgLysLeu 80
Db 311 GCACCTGTGACAGAGATGATCTGTCTTCCGACGGGCGCCCTTATTTACCGAAAGCTTCTG 370

Qy 81 PheAsnProSerGlyProTyrrGlnLysLysProValHisGlnLysGlyValLeu 99
Db 371 TTCAATCCAGCGGTCTCTTACGAAAGCCTGTGATATAAAGAAAGATTGTTG 427

RESULT 5

;; PRIOR APPLICATION NUMBER: 60/043,580
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,568
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,314
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,569
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,311
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,671
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,674
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,669
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,312
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,313
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,672
;; PRIOR FILING DATE: 1997-04-11
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;; PRIOR FILING DATE: 1997-04-11
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,636
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,874
;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,892
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/057,761

;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-05-23
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;; PRIOR FILING DATE: 1997-05-23
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,908
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/048,964
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/057,650
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/056,884
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/057,669
;; PRIOR FILING DATE: 1997-09-05

Alignment Scores:

;; Pred. No.: 6,68e-64 Length: 504
;; Score: 508.00 Matches: 99
;; Percent Similarity: 100.00% Conservative: 0
;; Best Local Similarity: 100.00% Mismatches: 0
;; Query Match: 100.00% Indels: 0
;; DB: 13 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-882-171-98 (1-504)

Oy 1 MetAspAsnValGlnProLysIleTySH1sArgProPhaCysPheSerValIysGlyH1s 20
Db 131 ATGATTAACCTGACGCGAAATAAACAATCGCCCTTGTGCTCACTGTAAGCCAC 190
Oy 21 ValIysMetIeuArgIeuAepIleIleAsnSerIeuValThrValIshMetIeuIle 40
Db 191 GTGAAGATGCTGGCTGATATTATCACTCACTGTAACAACAGTATTCAATGCTCATC 250

PRIOR APPLICATION NUMBER: 60/043,671
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,674
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PRIOR APPLICATION NUMBER: 60/043,313
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PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05

Alignment Scores:

Fred. No.: 6,72e-64 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dbs: 13 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-882-171-252 (1-506)

Qy 1 MetAspAsnValAlaGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 117 ATGATTAACGTGCAGCGGAATAAATCAATCGCCCTTGTGCTGATGGAAGCCAC 176
Qy 21 ValLysMetLeuLysLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 177 GTGAAGATGCTGGCGGTGATATTATCACTGATCAACAAGATTCATGCTCATC 236
Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAlaPhe 60
Db 237 GTATCTGTGTTGGACGATGACCAAGAACCAACATTCAGTTGGAGGGGTGTTT 236
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
Db 297 GCACCTTGACACGACGATGCTGTCTTCCGACGGGGCCCTTTATTACCGGAAGCTTCTG 356
Qy 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGlnLysGlnValLeu 99

Db 357 TTCATCCAGCGGCTCTTACAGAAAAAGCTGTGATGAAAAAGAGTTTG 413

RESULT 8

US-09-801-115-1

Sequence 1, Application US/09801115

Patent No. US2002001828A1

GENERAL INFORMATION:

APPLICANT: Ma, D.

APPLICANT: Han, W.

APPLICANT: Zhang, Y.

APPLICANT: Song, Q.

APPLICANT: Di, C.

APPLICANT: Huang, J.

APPLICANT: Tang, J.

APPLICANT: Chen, G.

TITLE OF INVENTION: CHEMOKINE LIKE FACTOR (CKLF) WITH CHEMOTACTIC AND HEMATOPOIETIC

TITLE OF INVENTION: STIMULATING ACTIVITIES

FILE REFERENCE: 10776-003-999

CURRENT APPLICATION NUMBER: US/09/801,115

CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: PCT/CN00/00026

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 99107284.7

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 1

LENGTH: 534

TYPE: DNA

ORGANISM: Homo sapiens

US-09-801-115-1

Alignment Scores:

Pred. No.:	7,29e-64	Length:	534
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-801-115-1 (1-534)

Qy 1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20

Db 152 ATGGATTAACGTCGACGCCGAAATTAACATGCCCCCTTCTGCTTCAAGTGAAAGGCCAC 211

Qy 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

Db 212 GTGAAGATGCTGCGCGCTGATATTATCAACTCAGCTGTAAACAAGATATTCATGCTCATC 271

Qy 41 ValSerValIleuAlaIleuIleProGluThrThrLeuThrValGlyGlyValPhe 60

Db 272 GTATCTGTGTGGACGATGATACCAAGAACCAACATTTGAGTGTGGAGGGGTGTTT 331

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyArgLysLeu 80

Db 332 GCACTTGTGACAGCAGTATGCTGCTTCCGACGGGGCCCTTATTACCGAAGCTTCTG 391

Qy 81 PheAsnProSerGlyProTyArgLysLeuProValHisGluLysGluValIleu 99

Db 392 TTCATCCAGCGGCTCTTACAGAAAAAGCTGTGATGAAAAAGAGTTTG 448

RESULT 9

US-10-106-698-1927

Sequence 1927, Application US/10106698

Patent No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA00501

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentm Ver. 3.0

SEQ ID NO 1927

LENGTH: 558

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (514)..(514)

OTHER INFORMATION: n equals a,t,g, or c

US-10-106-698-1927

Alignment Scores:

Pred. No.:	7,78e-64	Length:	558
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-801-115B-2 (1-99) x US-10-106-698-1927 (1-558)

Qy 1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20

Db 147 ATGGATTAACGTCGACGCCGAAATTAACATGCCCCCTTCTGCTTCAAGTGAAAGGCCAC 206

Qy 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

Db 207 GTGAAGATGCTGCGCGCTGATATTATCAACTCAGCTGTAAACAAGATATTCATGCTCATC 266

Qy 41 ValSerValIleuAlaIleuIleProGluThrThrLeuThrValGlyGlyValPhe 60

Db 267 GTATCTGTGTGGACGATGATACCAAGAACCAACATTTGAGTGTGGAGGGGTGTTT 326

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyArgLysLeu 80

Db 327 GCACTTGTGACAGCAGTATGCTGCTTCCGACGGGGCCCTTATTACCGAAGCTTCTG 386

Qy 81 PheAsnProSerGlyProTyArgLysLeuProValHisGluLysGluValIleu 99

Db 387 TTCATCCAGCGGCTCTTACAGAAAAAGCTGTGATGAAAAAGAGTTTG 443

RESULT 10

US-10-291-172-13

Sequence 13, Application US/10291172

Patent No. US20030228584A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-045

CURRENT APPLICATION NUMBER: US/10/291,172

CURRENT FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: 09/693,267

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/665,363

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 09/616,847

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 09/596,193

PRIOR FILING DATE: 2000-06-17

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 752

SEQ ID NO 13

LENGTH: 655

TYPE: DNA

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (134)..(430)
US-10-291-172-13

Alignment Scores:
Pred. No.: 9,89e-64 Length: 655
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-801-115B-2 (1-99) x US-10-291-172-13 (1-655)

QY 1 MetAspAsnValGlnProIysIleIySHsArGProPhCySPhSeSerValIySGIyHs 20
Db 134 ATGGATACGTGACGCCGAAATTAACATCGCCCTTCTGCTTCACTGTAAGGCGCAC 193
QY 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 194 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACACAGATTTCATCTCATC 253
QY 41 ValSerValIleuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
Db 254 GTATCTGTGTGGCAGTACGATACCAAGAACCAACATTGACAGTGTGGAGGGGTGTTT 313
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArgIysLeu 80
Db 314 GCACCTGTGACAGACGATATGCTGTTCGCCGACGGGCCCTTATTATTCGGAAGCTTCTG 373
QY 81 PheAsnProSerGlyProTyrrGlnIySLySProValHisGluIySLySGIuValLeu 99
Db 374 TTCATTCGCCAGCGGTCTTACACGAAAGAGCTGTGATGAAAAAGAGATTG 430

RESULT 11
US-10-119-428-14
Sequence 14, Application US/10119428
Publication No. US20030165881A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Wehman, Tom
APPLICANT: Ren, Feiyan
APPLICANT: Ma, Yungqing
APPLICANT: Zhou, Ping
APPLICANT: Zhao, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Dmanac, Radjic T.
TITLE OF INVENTION: No. US20030165881A1 Nucleic Acids and
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119,428
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: pc_fll_genes Version 1.0
SEQ ID NO 14
LENGTH: 817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (236)..(535)
US-10-119-428-14
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Alignment Scores:
Pred. No.: 1,38e-63 Length: 817
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-801-115B-2 (1-99) x US-10-119-428-14 (1-817)

QY 1 MetAspAsnValGlnProIysIleIySHsArGProPhCySPhSeSerValIySGIyHs 20
Db 236 ATGGATACGTGACGCCGAAATTAACATCGCCCTTCTGCTTCACTGTAAGGCGCAC 295
QY 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 296 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACACAGATTTCATCTCATC 355
QY 41 ValSerValIleuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
Db 356 GTATCTGTGTGGCAGTACGATACCAAGAACCAACATTGACAGTGTGGAGGGGTGTTT 415
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArgIysLeu 80
Db 416 GCACCTGTGACAGACGATATGCTGTTCGCCGACGGGCCCTTATTATTCGGAAGCTTCTG 475
QY 81 PheAsnProSerGlyProTyrrGlnIySLySProValHisGluIySLySGIuValLeu 99
Db 476 TTCATTCGCCAGCGGTCTTACACGAAAGAGCTGTGATGAAAAAGAGATTG 532

RESULT 12
US-09-918-995-19489
Sequence 19489, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19489
LENGTH: 512
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(512)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19489

Alignment Scores:
Pred. No.: 5,08e-63 Length: 512
Score: 502.00 Matches: 98
Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 1
Query Match: 98.82% Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-918-995-19489 (1-512)

QY 1 MetAspAsnValGlnProIysIleIySHsArGProPhCySPhSeSerValIySGIyHs 20
Db 142 ATGGATACGTGACGCCGAAATTAACATCGCCCTTCTGCTTCACTGTAAGGCGCAC 201
QY 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 202 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACACAGATTTCATCTCATC 261
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Qy      41 ValSeValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
Db      262 GRRTCGTGTGGCACTGATACCAAAACCAACATTCGACGTGGACGGGCTTT 321
Qy      61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArgLysLeuLeu 80
Db      322 GCACCTGTGTACAGCACTATGTCTGTCTGGCCGACGGGGCCCTTATTAACGGAACTTCTG 381
Qy      81 PheAsnProSerGlyProTyrrGluLysProValHisGluLysGluValLeu 99
Db      382 TTCAAATCCACGCGCTCTTACCAAGAAAAGCCTGTGATGAAAAAANAAGAGTTTGG 438

RESULT 13
US-10-319-763-53
Sequence 53, Application US/10319763
Publication No.: US20030144490A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 53
LENGTH: 500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 198..288
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.59999990463257
OTHER INFORMATION: seq IVSVALIBETTT/LT
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 464..469
FEATURE:
NAME/KEY: polyA_site
LOCATION: 489..500
FEATURE:
NAME/KEY: misc feature
LOCATION: 197..412
OTHER INFORMATION: homology
OTHER INFORMATION: id :AA429945
OTHER INFORMATION: est
FEATURE:
NAME/KEY: misc feature
LOCATION: 61..105
OTHER INFORMATION: homology
OTHER INFORMATION: id :AA429945
OTHER INFORMATION: est
FEATURE:
NAME/KEY: misc feature
LOCATION: 425..488
OTHER INFORMATION: homology
OTHER INFORMATION: id :AA429945
OTHER INFORMATION: est

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FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 197..412	
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NAME/KEY: misc_feature	
LOCATION: 425..488	
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LOCATION: 425..488	
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NAME/KEY: misc_feature	
LOCATION: 52..195	
OTHER INFORMATION: homology	
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NAME/KEY: misc_feature	
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LOCATION: 443..477	
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NAME/KEY: misc_feature
LOCATION: 197..338
OTHER INFORMATION: homology
OTHER INFORMATION: id:M52820
FEATURE:
NAME/KEY: misc_feature
LOCATION: 71..195
OTHER INFORMATION: homology
OTHER INFORMATION: id:M52820
OTHER INFORMATION: est
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..401
OTHER INFORMATION: homology
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NAME/KEY: misc_feature
LOCATION: 425..469
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LOCATION: 40..195
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OTHER INFORMATION: est
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NAME/KEY: misc_feature
LOCATION: 9..10,12
OTHER INFORMATION: n=a, g, c or t
US-10-319-763-53
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Alignment Scores:
Pred. No.: 3,77e-61 Length: 500
Score: 489.00 Matches: 98
Percent Similarity: 98.00% Conservative: 0
Best Local Similarity: 98.00% Mismatches: 1
Query Match: 96.26% Indels: 1
DB: Gaps: 0
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US-09-801-115b-2 (1-99) x US-10-319-763-53 (1-500)

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QY 1 MetAspAsnValGlnProIysIleIysHisArgProPhCySpheSerValIysGlyHis 20
DB 132 ATGATTAACGTGACGCGGAAATTAACATCGCCCTTCTGCTTCACTGTGAAGGCCAC 191
QY 21 ValMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeu 40
DB 192 GTGATGATGCTGGCGCTGATATTAACAACCAACCAACCAACCAACCAACCAACCAAC 251
QY 40 eValSerValIleuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
DB 252 CGATATCTGTGGCACTGATACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 311
QY 60 eAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleArgIysLeu 80
DB 312 TGCACTGTGACAGCAGTATGCTCTCTTGGCGAGGGGCCCTTATTACCGGAGCTTCT 371
QY 80 upheAsnProSerGlyProIleGlnIysIysProValHisGlnIysIysGlnValLeu 99
DB 372 GTTCAATCCAGCGGCTCTTACCAAGAAAGAGCTGTGCAAGAAAGAAAGAGCTTTTG 429
RESULT 14
US-10-242-535A-7940
; Sequence 7940, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Lew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
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FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7940
LENGTH: 400
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (176)..(176)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-7940
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Pred. No.: 7.91e-59 Length: 400
Score: 472.00 Matches: 94
Percent Similarity: 97.92% Conservative: 0
Best Local Similarity: 97.92% Mismatches: 1
Query Match: 92.91% Indels: 1
DB: Gaps: 0
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US-09-801-115b-2 (1-99) x US-10-242-535A-7940 (1-400)

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QY 21 ValMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeu 40
DB 175 GNGAAGATGCTGGCGCTGATATTAACAACCAACCAACCAACCAACCAACCAACCAAC 234
QY 41 ValSerValIleuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
DB 235 GTATCTGTGTTGCACTGATACCAAGAAACCAACCAACCAACCAACCAACCAACCAAC 294
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleArgIysLeu 80
DB 295 GCACCTGTGACGAGTATGCTCTTGGCGAGGGGCCCTTATTACCGGAGCTTCT 354
QY 80 upheAsnProSerGlyProIleGlnIysIysProValHisGlnIys 95
DB 355 GTTCAATCCAGCGGCTCTTACCAAGAAAGAGCTGTGCAAGAAAGAGAGCTTTTG 400
RESULT 15
US-09-801-115-3
; Sequence 3, Application US/09801115
; Patent No. US20020001828A1
; GENERAL INFORMATION:
; APPLICANT: Ma, D.
; APPLICANT: Han, W.
; APPLICANT: Zhang, Y.
; APPLICANT: Song, Q.
; APPLICANT: Di, C.
; APPLICANT: Huang, J.
; APPLICANT: Tang, J.
; APPLICANT: Chen, G.
; TITLE OF INVENTION: CHEMOKINE LIKE FACTOR (CLF) WITH CHEMOTACTIC AND HEMATOPOIETIC
; FILE REFERENCE: 10776-003-999
; CURRENT APPLICATION NUMBER: US/09/801,115
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/CN00/00026
; PRIOR FILING DATE: 2000-02-15
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? PRIOR APPLICATION NUMBER: 99107284.7
 ? PRIOR FILING DATE: 1999-05-14
 ? NUMBER OF SEQ ID NOS: 8
 ? SEQ ID NO 3
 ? LENGTH: 459
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-801-115-3

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Length:	459
Score:	471.50
Percent Similarity:	65.13%
Best local Similarity:	65.13%
Query Match:	92.81%
DB:	9
Gaps:	1

US-09-801-115B-2 (1-99) x US-09-801-115-3 (1-459)

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Qy	21 ValIysMetLeuArg	25
Db	61 GTGAAGATGCTGGGCTGGCAGCTAACTGACATCTATGACCTTTTATCATGCACAA	120
Qy	25 -----	25
Db	121 GCCCCTGAACCATATATTTGTATCACTGAGTTTGAAGTACCGTTACTTATTTTTCATA	180
Qy	26 -----	LeuAsp 27
Db	181 CTTTATATGTAAGTACGACTGTGATGATTAATGAAGTGGTATATTGGCTTTGCTTGAT	240
Qy	28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle	47
Db	241 ATTATCAACTCATCTGTAAACAACAGTATTCACATCGATCGATCGTGTGGCACTATA	300
Qy	48 ProGluThrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCys	67
Db	301 CCGAAGAACCAACATTTGACAGTGTGGAGGGGCTTTGCACTTTGTACACGACTATGC	360
Qy	68 CysLeuAlaAspGluValaLeuIleTyrArgIysLeuLeuPheAsnProSerGlyProTyr	87
Db	361 TGTCTTGGCGACGGGGCCCTTATTTTACCGGAAGCTTCTGTTCATCCACGAGGTCCTTAC	420
Qy	88 GlnIlySerProValHisGluIysIysGluValaLeu	99
Db	421 CAGAAAAAGCTGTGCATAAAAAAGAAAGTTTGG	456

Search completed: January 31, 2004, 05:31:41
Job time : 275 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2004, 04:11:13 ; Search time 74 Seconds
(without alignments)
590.499 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR MAX=pct -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	508	100.0	413	4	US-09-663-600A-147
2	508	100.0	504	4	US-09-149-476-98
3	508	100.0	506	4	US-09-149-476-252
4	508	100.0	515	4	US-09-599-360B-29
5	491	96.7	526	4	US-09-220-132-164
6	489	96.3	500	4	US-09-663-600A-53
7	471.5	92.8	669	4	US-09-599-360B-70
8	357	70.3	392	3	US-09-385-982-95
9	83	16.3	37948	3	US-09-251-646-11
10	73	14.4	1083	3	US-09-116-498-11
11	73	14.4	1083	4	US-09-170-496D-179
12	71	14.0	1083	3	US-09-116-498-7

13	71	14.0	1083	4	US-09-170-496D-27	Sequence 27, Appl
14	71	14.0	1232	4 <th>US-09-016-434-1079</th> <th>Sequence 1079, Ap</th>	US-09-016-434-1079	Sequence 1079, Ap
15	66.5	13.1	720	1 <th>US-08-061-092A-2</th> <th>Sequence 2, Appl1</th>	US-08-061-092A-2	Sequence 2, Appl1
16	66	13.0	4403765	3 <th>US-09-103-840A-2</th> <th>Sequence 1, Appl1</th>	US-09-103-840A-2	Sequence 1, Appl1
17	66	13.0	4411529	3 <th>US-09-103-840A-1</th> <th>Sequence 12, Appl</th>	US-09-103-840A-1	Sequence 12, Appl
18	65.5	12.9	43676	3 <th>US-09-356-952-12</th> <th>Sequence 1, Appl1</th>	US-09-356-952-12	Sequence 1, Appl1
19	65	12.8	3872	4 <th>US-09-165-396-1</th> <th>Sequence 9, Appl1</th>	US-09-165-396-1	Sequence 9, Appl1
20	64.5	12.7	1333	1 <th>US-08-684-862-9</th> <th>Sequence 1, Appl1</th>	US-08-684-862-9	Sequence 1, Appl1
21	64.5	12.7	2211	3 <th>US-09-462-844-1</th> <th>Sequence 14, Appl</th>	US-09-462-844-1	Sequence 14, Appl
22	64.5	12.7	7721	3 <th>US-08-772-770A-14</th> <th>Sequence 1, Appl1</th>	US-08-772-770A-14	Sequence 1, Appl1
23	64.5	12.7	1664976	4 <th>US-08-916-421B-1</th> <th>Sequence 1, Appl1</th>	US-08-916-421B-1	Sequence 1, Appl1
24	64	12.6	1278	4 <th>US-09-107-532A-2920</th> <th>Sequence 2920, Ap</th>	US-09-107-532A-2920	Sequence 2920, Ap
25	64	12.6	17710	4 <th>US-08-976-359-70</th> <th>Sequence 70, Appl</th>	US-08-976-359-70	Sequence 70, Appl
26	64	12.6	25165	4 <th>US-09-453-702B-39</th> <th>Sequence 39, Appl</th>	US-09-453-702B-39	Sequence 39, Appl
27	63.5	12.5	654	3 <th>US-08-998-416-176</th> <th>Sequence 176, App</th>	US-08-998-416-176	Sequence 176, App
28	63.5	12.5	1785	4 <th>US-09-377-155-8</th> <th>Sequence 8, Appl1</th>	US-09-377-155-8	Sequence 8, Appl1
29	63.5	12.5	1785	4 <th>US-09-669-974-8</th> <th>Sequence 8, Appl1</th>	US-09-669-974-8	Sequence 8, Appl1
30	63.5	12.5	2153	4 <th>US-09-367-206-6</th> <th>Sequence 6, Appl1</th>	US-09-367-206-6	Sequence 6, Appl1
31	63	12.4	1818	4 <th>US-09-252-991A-7778</th> <th>Sequence 7778, Ap</th>	US-09-252-991A-7778	Sequence 7778, Ap
32	63	12.4	1854	1 <th>US-08-249-420-1</th> <th>Sequence 1, Appl1</th>	US-08-249-420-1	Sequence 1, Appl1
33	63	12.4	1854	2 <th>US-08-737-663-1</th> <th>Sequence 1, Appl1</th>	US-08-737-663-1	Sequence 1, Appl1
34	63	12.4	2241	4 <th>US-09-252-991A-7562</th> <th>Sequence 7562, Ap</th>	US-09-252-991A-7562	Sequence 7562, Ap
35	63	12.4	4403765	3 <th>US-09-103-840A-2</th> <th>Sequence 2, Appl1</th>	US-09-103-840A-2	Sequence 2, Appl1
36	63	12.4	4411529	3 <th>US-09-103-840A-1</th> <th>Sequence 1, Appl1</th>	US-09-103-840A-1	Sequence 1, Appl1
37	62.5	12.3	615	4 <th>US-09-134-001C-376</th> <th>Sequence 376, App</th>	US-09-134-001C-376	Sequence 376, App
38	62.5	12.3	1105	4 <th>US-09-221-017B-108</th> <th>Sequence 108, App</th>	US-09-221-017B-108	Sequence 108, App
39	62.5	12.3	9711	4 <th>US-08-961-527-167</th> <th>Sequence 167, App</th>	US-08-961-527-167	Sequence 167, App
40	62	12.2	745	4 <th>US-09-221-017B-319</th> <th>Sequence 319, App</th>	US-09-221-017B-319	Sequence 319, App
41	62	12.2	819	1 <th>US-08-309-182B-2</th> <th>Sequence 2, Appl1</th>	US-08-309-182B-2	Sequence 2, Appl1
42	62	12.2	6943	4 <th>US-09-453-702B-213</th> <th>Sequence 213, App</th>	US-09-453-702B-213	Sequence 213, App
43	61.5	12.1	1327	6 <th>5320941-1</th> <th>Patent No. 5320941</th>	5320941-1	Patent No. 5320941
44	61.5	12.1	1435	2 <th>US-08-878-989-14</th> <th>Sequence 14, Appl</th>	US-08-878-989-14	Sequence 14, Appl
45	61.5	12.1	1435	3 <th>US-09-272-796-14</th> <th>Sequence 14, Appl</th>	US-09-272-796-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-663-600A-147
; Sequence 147, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouguerelet, Lydie
; TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 147
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig.peptide
; LOCATION: 46..189
; OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 4.09999990463257
OTHER INFORMATION: seq VFMLIVSLALIP/ET
NAME/KEY: polyA signal
LOCATION: 377..382
NAME/KEY: polyA site
LOCATION: 402..413
US-09-663-600A-147

Alignment Scores:
Pred. No.: 2,33e-66 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 4

US-09-801-115B-2 (1-99) x US-09-663-600A-147 (1-413)

QY 1 MetaspasnaValGlnProlysiIeIyshiArgProPhcCypheserVallysglyhis 20
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QY 21 VallyshmetleuAsgleuAselelleAsnSerleuValThrThrValPheMetleuile 40
Db 106 GTGAAGAGTGGCGCGCTGATATTATCACTGATGTAACACAGATTTCATGCTCATC 165

QY 41 ValserValleuAlaIeulIeProgluThrThrleuThrValGlyGlyValPhe 60
Db 166 GTACTCTGTTGGACGATGATCCGAAACCAACATTGACAGTGTGAGGGGTCTT 225

QY 61 AlaIeuValThrAlaValCysCysleuAlaAspGlyAlaIeuIeYrArglyleu 80
Db 226 GCACTGTGACAGCAGTATGCTGCTGCGACGCGGCCCTTATTACCGAAGCTTCTG 285

QY 81 PheAspProserGlyProTyrglnIlyseIyProValHisgluIylysglyValIeu 99
Db 286 TTCAATCCAGCGGTCTTACCAAGAAAGCCTGTGATGAAAAAAGAGTTT 342

RESULT 2
US-09-149-476-98
Sequence 98. Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149, 476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
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EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878

EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
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EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Alignment Scores:
Pred. No.: 3,14e-66 Length: 504
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-149-476-98 (1-504)

QY 1 MetAspAsnValGlnProIysIleIysHISarxProPheCysPheSerValIysGlyHIS 20
DB 131 ATGGATTAACCTGACGCCGAAATATAAATCATGCCCTTCTGCTTCTGATGGAAGGCCAC 190

QY 21 ValIysMetLeuArgIleuAspIleIleAsnSerLeuValThrThyValPheMetLeuIle 40
DB 191 GTGAAGATGTGGGGCTGGATATTATCACTCACTGTTAAACAACAGATTATCATGTCATC 250

QY 41 ValSerValIleuAlaLeuIleProGluThrThrThleuThyValGlyValPhe 60
DB 251 GTATCTGTGTGGACATGATACCAAGAACCAACAATTGACAGTTGGTGGAGGGGCTTT 310

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArgIysLeu 80
DB 311 GCACCTGTGACACAGATATGCTGTCTGGCCGAGGGGCCCTTATTTACCGAAGCTTCTG 370

QY 81 PheAsnProSerGlyProTyrGlnIysIysProValHISGluIysIysGluValLeu 99
DB 371 TTCAATCCACGGCGTCTTACCAAGAAAAGCCGTGTCATGAATAAAGAAAGTTTG 427

RESULT 3
US-09-149-476-252
Sequence 252, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002PI
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334

[illegible]

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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
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EARLIER APPLICATION NUMBER: 60/056,909
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EARLIER APPLICATION NUMBER: 60/056,875
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EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Alignment Scores:
Pred. No.: 3,15e-66 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-801-115B-2 (1-99) x US-09-149-476-252 (1-506)

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QY 1 MetAspAsnValAlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 117 ATGGATTAACGTGCAGCGGAAATTAACATCGCCCTTCTGCTTCAAGTGAAGGCCAC 176
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 177 GTGAAGATGCTGCGCTGGATATTATCACTGCTGTAACAACAGATTTCATCTATC 236
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 237 GTACTCTGTGGTGGACATGATCCAGAAACCAACATTGACAGTGTGGAGGGGTCTT 296
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
Db 297 GCACCTGTGACAGAGATATGCTGCTTGCAGCGGGCCCTTATTATCCGGAACCTTCTG 356
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluValLysGluValLeu 99
Db 357 TTCAATCCACGCGGTCTTACCAAGAAAGCCGTGTGATGAAAAAGAGTTTGG 413
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```
RESULT 4
US-09-599-3608-29
; Sequence 29, Application US/095993608
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueteloret, L.
```

```
APPLICANT: Ubert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 29
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..440
; NAME/KEY: sig_peptide
; LOCATION: 144..287
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.10
; NAME/KEY: polyA_signal
; LOCATION: 457..462
; NAME/KEY: polyA_site
; LOCATION: 500..515
; NAME/KEY: misc_feature
; LOCATION: 60
; OTHER INFORMATION: n=a, g, c or t
US-09-599-3608-29
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Alignment Scores:
Pred. No.: 3,24e-66 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-801-115B-2 (1-99) x US-09-599-3608-29 (1-515)

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QY 1 MetAspAsnValAlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 144 ATGGATTAACGTGCAGCGGAAATTAACATCGCCCTTCTGCTTCAAGTGAAGGCCAC 203
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 204 GTGAAGATGCTGCGCTGGATATTATCACTGCTGTAACAACAGATTTCATCTATC 263
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 264 GTACTCTGTGGTGGACATGATCCAGAAACCAACATTGACAGTGTGGAGGGGTCTT 323
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
Db 324 GCACCTGTGACAGAGATATGCTGCTTGCAGCGGGCCCTTATTATCCGGAAGCTTCTG 383
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluValLysGluValLeu 99
Db 384 TTCAATCCACGCGGTCTTACCAAGAAAGCCGTGTGATGAAAAAGAGTTTGG 440
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RESULT 5
US-09-220-132-164/c
; Sequence 164, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
```

;; CURRENT APPLICATION NUMBER: US/09/220,132
;; CURRENT FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: US 60/079,303
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: US 60/068,821
;; PRIOR FILING DATE: 1997-12-24
;; NUMBER OF SEQ ID NOS: 191
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 164
;; LENGTH: 526
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(526)
;; OTHER INFORMATION: n = A,T,C or G
US-09-220-132-164

Alignment Scores:
Pred. No.: 1,12e-63 Length: 526
Score: 491.00 Matches: 98
Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 0
Query Match: 96.65% Indels: 1
DB: 4 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-220-132-164 (1-526)

QY 1 MetaspantValGlnProlylIlelyshisArg-ProthecypheserVallysglyhi 20
DB 370 ATGGATACGTCGACGCCAATAAATACATCGGCCCTTCCTTCATGTGAAGGCCA 311
QY 20 Gvallyswetleuargleuaapilleleasnserleuvalthrthrvalphemetteu 40
DB 310 CGTGAAGATGCTGCGCGCTGGAATATTATCACTCACTGTAACAACAGATTCACTCAT 251
QY 40 evalserValleuValleuileprogluThrThrThrleuThrValglyglyValph 60
DB 250 CGTATCTGTGTGGCAGTATACCAAGAACCAACATGACAGTGTGAGGGGTGT 191
QY 60 ealaleuValthrValvalcyGcyGleuValaaspGlyValaleuiletyrAglyleu 80
DB 190 TGCACCTGTGACAGCAGATGCTGTCTGCGACGGGGCCCTTATTATACCGAAGCTTCT 131
QY 80 uPhaasnProserGlyProTyrglnlyValProValhIsGluylsglyVal 98
DB 130 GTTCATCCAGCGGCTCTTACCAAGAAAGCGTGTGATGAAAAAAGAGATT 76

RESULT 6
US-09-663-600A-53
;; Sequence 53, Application US/09663600A
;; Patent No. 6573068
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;; APPLICANT: Duclert, Aymeric
;; APPLICANT: Bousquelert, Lydie
;; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
;; FILE REFERENCE: 31.US3.CTP
;; CURRENT APPLICATION NUMBER: US/09/663,600A
;; CURRENT FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 09/191,997
;; PRIOR FILING DATE: 1998-11-13
;; PRIOR APPLICATION NUMBER: 60/066,677
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/069,957
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/074,121
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/081,563
;; PRIOR FILING DATE: 1998-04-13
;; PRIOR APPLICATION NUMBER: 60/096,116
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/099,273

;; PRIOR FILING DATE: 1998-09-04
;; NUMBER OF SEQ ID NOS: 229
;; SOFTWARE: Patent.pm
;; SEQ ID NO 53
;; LENGTH: 500
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 199..288
;; OTHER INFORMATION: Von Heijne matrix
;; OTHER INFORMATION: score 5.59999990463257
;; OTHER INFORMATION: seq IVSVLALIPETTT/LT
;; NAME/KEY: polyA_signal
;; LOCATION: 464..469
;; NAME/KEY: polyA_site
;; LOCATION: 489..500
;; NAME/KEY: misc_feature
;; LOCATION: 197..412
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA429945
;; NAME/KEY: misc_feature
;; LOCATION: 61..195
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA429945
;; NAME/KEY: misc_feature
;; LOCATION: 197..412
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA455042
;; NAME/KEY: misc_feature
;; LOCATION: 61..195
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA455042
;; NAME/KEY: misc_feature
;; LOCATION: 425..488
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA455042
;; NAME/KEY: misc_feature
;; LOCATION: 207..412
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: W93646
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 58..195
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: W93646
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 425..468
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: W93646
;; NAME/KEY: misc_feature
;; LOCATION: 197..412
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA516431
;; NAME/KEY: misc_feature
;; LOCATION: 90..195
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA516431
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature


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LOCATION: 425..488
OTHER INFORMATION: homology
OTHER INFORMATION: id :AA516431
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 52..195
OTHER INFORMATION: homology
OTHER INFORMATION: id :W38899
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 197..334
OTHER INFORMATION: homology
OTHER INFORMATION: id :W38899
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 443..477
OTHER INFORMATION: homology
OTHER INFORMATION: id :W38899
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 197..338
OTHER INFORMATION: homology
OTHER INFORMATION: id :W52820
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 71..195
OTHER INFORMATION: homology
OTHER INFORMATION: id :W52820
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 339..401
OTHER INFORMATION: homology
OTHER INFORMATION: id :W52820
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 425..469
OTHER INFORMATION: homology
OTHER INFORMATION: id :W52820
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 40..195
OTHER INFORMATION: homology
OTHER INFORMATION: id :W19506
OTHER INFORMATION: est
NAME/KEY: misc.feature
LOCATION: 9..10,12
OTHER INFORMATION: n=a, g, c or t
US-09-663-600A-53

Alignment Scores:
Pred. No.: 2,05e-63
Score: 489.00
Percent Similarity: 98.00%
Best Local Similarity: 98.00%
Query Match: 96.26%
Length: 500
Matches: 98
Conservative: 0
Mismatch: 1
Indels: 1
Gaps: 0

US-09-801-115B-2 (1-99) x US-09-663-600A-53 (1-500)
Qy 1 MetAspAnValGlnProLysIleLysHisArgProPheCysPheSerValIysGlyHis 20
Db 132 ATGATTAACGTGCAGCCGAAATTAACATCGCCCTTCCTTCAGTGTAAGGCGCAC 191
Qy 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuI 40
Db 192 GTGAGAGTGTCTGGCGGTGATATATCACTCACTGTAAACAAGATTCATGCTCAT 251
Qy 40 eValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPh 60
Db 252 CTTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTTGGAGAGGGGTGTT 311
Qy 60 eAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraGlySLeu 80
Db 60 eAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraGlySLeu 80
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Db 312 TGCACTTGACAGCAGTATGCTGCTGCCACAGGGGCCCTTATTTACCGAAGCTTC 371
Qy 80 uPheAnProSerGlyProTyGlnLysLysProValHisGluLysGlyValLeu 99
Db 372 GTTCATCCAGCGGCTTACCAAGAAAAAGCTGTGATGAAAAAAGAACTTTTG 429

RESULT 7
US-09-599-360B-70
Sequence 70, Application US/09599360B
Patent No. 654863
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bouquelere, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET.0500C3
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 70
LENGTH: 669
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 140..595
NAME/KEY: sig.peptide
LOCATION: 140..442
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.10
NAME/KEY: polyA.signal
LOCATION: 630..635
NAME/KEY: polyA.site
LOCATION: 655..669
US-09-599-360B-70

Alignment Scores:
Pred. No.: 1,26e-60
Score: 471.50
Percent Similarity: 65.13%
Best Local Similarity: 92.81%
Query Match: 4
Length: 669
Matches: 99
Conservative: 0
Mismatch: 53
Indels: 1
Gaps: 1

US-09-801-115B-2 (1-99) x US-09-599-360B-70 (1-669)
Qy 1 MetAspAnValGlnProLysIleLysHisArgProPheCysPheSerValIysGlyHis 20
Db 140 ATGATTAACGTGCAGCCGAAATTAACATCGCCCTTCCTTCAGTGTAAGGCGCAC 199
Qy 21 ValLysMetLeuArg----- 25
Db 200 GTGAGAGTGTCTGGCGGTGACCTAATGATGACATCTATGACCTTTTATCATCGACAA 259
Qy 25 ----- 25
Db 260 GCCCGTAACCATATATTTGTTATCACTGCAATTGAAGTCAACCGTTATCTTATTTTCATA 319
Qy 26 -----LeuAsp 27
Db 320 CTTTATATGTAATCACTGATTCATTAATGAAGTGTATTTGGCCTTGTGAT 379
Qy 28 IleIleAsnSerLeuValThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
Db 380 ATTATCAACTCACTGATTAACCAAGATATTCATCTCATCTATCTGTGTGGCACTGATA 439
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QY 48 ProglutThrThrThrThrThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 440 CCAAGAACACACACATTGACAGTGTGTGAGGGGGTGTTCACCTTGACAGCAGTATGC 499
QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87
Db 500 TGTCTTGGCCGAGCGGGCCCTTATTTACCGAAGCTTCTGTTCAATCCACGCGCTTAC 559
QY 88 GlnLysLysProValHisGlnLysGlyGlyValLeu 99
Db 560 CAGAAAAGCCTGTGCAATGAAAAAAGAAAGTTTG 595
RESULT 8
US-09-385-982-95
; Sequence 95, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNDA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(392)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-95
Alignment Scores:
Pred. No.: 5,73e-44 Length: 392
Score: 357.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.28% Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x US-09-385-982-95 (1-392)
QY 26 LeuAspIleIleAsnSerLeuValThrValPheMetLeuIleValSerValLeuAla 45
Db 44 CTGTATATTATCACTCACTGATGTAACAACAGTATTCATGCTCATGCTGTGGCA 103
QY 46 LeuIleProGluThrThrThrThrValGlyGlyGlyValPheAlaLeuValThrAla 65
Db 104 CTGATACCAAGAACACACATTGACAGTGTGTGAGGGGGTGTTCACCTGTGACACCA 163
QY 66 ValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGly 85
Db 164 GTATCTCTCTTGGCGAGCGGGCCCTTATTTACCGAAGCTTCTGTTCAATCCACGCGGT 223
QY 86 ProTyrGlnLysLysProValHisGlnLysLys 96
Db 224 CTTTACCAAGAAAGCCTGTGCAATGAAAAA 256
RESULT 9
US-09-251-645-11
; Sequence 11, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:

; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 37948
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15171)..(18035)
; OTHER INFORMATION: orf5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23768)..(31336)
; OTHER INFORMATION: hph2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31393)..(35838)
; OTHER INFORMATION: orf2
US-09-251-645-11
Alignment Scores:
Pred. No.: 2.47 Length: 37948
Score: 83.00 Matches: 28
Percent Similarity: 51.76% Conservative: 16
Best Local Similarity: 32.94% Mismatches: 21
Query Match: 16.34% Indels: 20
Gaps: 5
US-09-801-115B-2 (1-99) x US-09-251-645-11 (1-37948)
QY 12 ProPheCysPheSerValLysGlyHisValLysMetLeuArgLeuAspIleIleAsnSer 31
Db 6476 CCAATATGCTTCTTAAAGAAATGACACCTGAATATCAAAACCTTATTAACAGT 6535
QY 32 LeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThrThr 51
Db 6536 TTGATTA---CTAATGATATTATGTTGCTCAATATGCTATGCAAGAAAGCTACGAAA 6589
QY 52 ThrLeu-----ThrValGlyGlyValPheAlaLeuValThrAla 65
Db 6590 TCCCTTCATGATTAATAGTAATAGTAACGCTTATGATGGGAGATGGCTATC-----TGA 6643
QY 66 ValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSer--- 84
Db 6644 GTATGGGTATGCGCGAA-----ATATTACGCATCAAAAC 6679
QY 85 ---GlyProTyrGln 88
Db 6680 TGGAGTCCATCATCAG 6694
RESULT 10
US-09-116-498-11
; Sequence 11, Application US/09116498
; Patent No. 6251582
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Deng, Hongkui
; APPLICANT: Unutmaz, Derya
; APPLICANT: Ramani, Vineet N.K.
; TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
; ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF

IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: pigtail macaque
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-116-498-11
Alignment Scores:
Pred. No.: 0.387 Length: 1083
Score: 73.00 Matches: 25
Percent Similarity: 39.33% Conservative: 10
Best Local Similarity: 28.09% Mismatches: 24
Query Match: 14.37% Indels: 30
Gaps: 3 4
US-09-801-115B-2 (1-99) x US-09-116-498-11 (1-1083)
QY 8 11eleYh1aRgProPhCySPhSeSeVallySgLyH1sVallySMeLLeuAArgLeuAasp 27
Db 529 ATTGATGATTAAGCCATCTGT-----GCAGAGAAAAGGCACTCCACTTAA 576
QY 28 11eleASeSeLeuValThrThrValPheMeLeuLeuValSeValLeuAlaLeuIle 47
Db 577 CTCATATGCGCCCTGCGCTTAATTTTCACTTTTGTCCCTTTGTTG----- 627
QY 48 ProGluThrThrThrLeuThrValIglyIglyValPheAlaLeuValThralaValCys 67
Db 628 -----AGCATGTGACCTGCTACTGT 648
QY 68 CyLeuAlaAspGlyAlaLeuIleTyRArgLySeuLeuPheAnProSeGlyProTyR 87
Db 649 TGCATTGCA-----AGGAGCTGTGTGCCAT-----TAC 678
QY 88 GlnLySlySProValHisGlyLySlys 96
Db 679 CAGCAGTCAGGAAGCAACAAAAAG 705
RESULT 11
US-09-170-496D-179
Sequence 179, Application US/09170496D

Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Law, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
SOFTWARE: Patent version 3.1
SEQ ID NO 179
LENGTH: 1083
TYPE: DNA
ORGANISM: Homo sapiens
US-09-170-496D-179
Alignment Scores:
Pred. No.: 0.387 Length: 1083
Score: 73.00 Matches: 25
Percent Similarity: 39.56% Conservative: 11
Best Local Similarity: 27.47% Mismatches: 27
Query Match: 14.37% Indels: 28
Gaps: 4 4
US-09-801-115B-2 (1-99) x US-09-170-496D-179 (1-1083)
QY 8 11eleYh1aRgProPhCySPhSeSeVallySgLyH1sVallySMeLLeuAArgLeuAasp 27
Db 529 ATTGATGATTAAGCCATCTGT-----GCAGAGAAAAGGCACTCCACTTAA 576
QY 28 11eleASeSeLeuValThrThrValPheMeLeuLeuValSeValLeuAlaLeuIle 47
Db 577 CTCATATGCGCCCTGCGCTTAATTTTCACTTTTGTCCCTTTGTTG----- 627
QY 48 ProGluThrThrThrLeuThrValIglyIglyValPheAlaLeuValThralaValCys 67
Db 628 -----AGCATGTGACCTGCTACTGT 648
QY 68 CyLeuAlaAspGlyAlaLeuIleTyRArgLySeuLeu-----PheAnProSeGly 85
Db 649 TGCATTGCA-----AGGAGCTGTGTGCCATTAACGACATCAGGA 690
QY 86 ProTyRGlnLySProValHisGlyLySlys 96
Db 691 AAGCACAACAAAAGCTGAAGAAATCTAAGAG 723
RESULT 12
US-09-116-498-7
Sequence 7, Application US/09116498
Patent No. 6251582
GENERAL INFORMATION:
APPLICANT: Littleman, Dan R.
APPLICANT: Deng, Hongkui
APPLICANT: Unutemaz, Derya
APPLICANT: Ramani, Vineet N K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-JUL-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-116-498-7

Alignment Scores:
Pred. No.: 0.766 Length: 1083
Score: 71.00 Matches: 24
Percent Similarity: 39.33% Conservative: 11
Best Local Similarity: 26.97% Mismatches: 24
Query Match: 13.98% Indels: 30
Gaps: 4

US-09-801-115B-2 (1-99) x US-09-116-498-7 (1-1083)

QY 8 ILeYsHsArGpRPhCysPheSeRvAllySGlyHsVallyMeLeuArgLeuAsp 27
Db 529 ATTGATGATAGCCATCTGT-----GCAGAGAAAAGCACAATCCCAATTAA 576
QY 28 ILeIeaNsErLeuValThrThValPheMeLeuIleValSerValLeuAlaLeuIle 47
Db 577 CTCATATGCTCCGTGGCTTAATTTTCACTTTTGTCCCTTGTG----- 627
QY 48 ProGUthrrThrThLeuthrValIGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 628 -----ACGATTGTGACCTGCTACTGT 648
QY 68 CysLeuAlaAspGlyAlaLeuIleTyraGlyLeuLeuPheAsnProSerGlyProTyr 87
Db 649 TGCATTGCA-----AGCAAGCTGTGTGCCAT-----TAC 678
QY 88 GlnYsLysProValHisGlnYsLys 96
Db 679 CAGCAATCAGAGAAAGCACACAAAAG 705

RESULT 13
US-09-170-496D-27
Sequence 27, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
LENGTH: 1083

TYPE: DNA
ORGANISM: Homo sapiens
US-09-170-496D-27

Alignment Scores:
Pred. No.: 0.766 Length: 1083
Score: 71.00 Matches: 24
Percent Similarity: 39.33% Conservative: 11
Best Local Similarity: 26.97% Mismatches: 24
Query Match: 13.98% Indels: 30
Gaps: 4

US-09-801-115B-2 (1-99) x US-09-170-496D-27 (1-1083)

QY 8 ILeYsHsArGpRPhCysPheSeRvAllySGlyHsVallyMeLeuArgLeuAsp 27
Db 529 ATTGATGATAGCCATCTGT-----GCAGAGAAAAGCACAATCCCAATTAA 576
QY 28 ILeIeaNsErLeuValThrThValPheMeLeuIleValSerValLeuAlaLeuIle 47
Db 577 CTCATATGCTCCGTGGCTTAATTTTCACTTTTGTCCCTTGTG----- 627
QY 48 ProGUthrrThrThLeuthrValIGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 628 -----ACGATTGTGACCTGCTACTGT 648
QY 68 CysLeuAlaAspGlyAlaLeuIleTyraGlyLeuLeuPheAsnProSerGlyProTyr 87
Db 649 TGCATTGCA-----AGCAAGCTGTGTGCCAT-----TAC 678
QY 88 GlnYsLysProValHisGlnYsLys 96
Db 679 CAGCAATCAGAGAAAGCACACAAAAG 705

RESULT 14
US-09-016-434-1079
Sequence 1079, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Setlamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1079:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 1232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1171145
;
US-09-016-434-1079

Alignment Scores:
Pred. No.: 0.927 Length: 1232
Score: 71.00 Matches: 24
Percent Similarity: 39.33% Conservative: 11
Best Local Similarity: 26.97% Mismatches: 24
Query Match: 13.98% Indels: 30
Gaps: 4

US-09-801-115B-2 (1-99) x US-09-016-434-1079 (1-1232)

QY 8 ILeYshIsArGpPheCysPheSeRvAllySgLYhIsVAllySMetLeuArGLeuAsp 27
Db 611 ATTGATGATAGACCATCTCTG-----GCAGAGAAAAGCACTCCATTAA 658
QY 28 ILeIeAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
Db 659 CTCATATGTCCTCGTGCGCTTATTTTCACCTTTTGTCTTGTCTTGTG----- 709
QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 710 -----AGCATGTGACCTGCTACTGT 730
QY 68 CysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeuPheAsnProSerGlyProTyr 87
Db 731 TGCATTGCA-----AGGAGCTGTGTGCCAT-----TAC 760
QY 88 GlnLysLysProValHisGlnLysLys 96
Db 761 CAGCAATCAGAAAGCACACAAAAG 787

RESULT 15
US-08-061-092A-2/c
; Sequence 2, Application US/08061092A
; Patent No. 5587458
; GENERAL INFORMATION:
; APPLICANT: KING, C R
; APPLICANT: KASPRZYK, Philip G
; APPLICANT: BIRD, Robert E
; TITLE OF INVENTION: ANTI-erbB-2 ANTIBODIES, COMBINATIONS
; TITLE OF INVENTION: THEREOF, AND THERAPEUTIC AND DIAGNOSTIC USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061.092A
; FILING DATE: 14-MAY-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuch, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 018797-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
;
US-08-061-092A-2

Alignment Scores:
Pred. No.: 1.95 Length: 720
Score: 66.50 Matches: 22
Percent Similarity: 48.61% Conservative: 13
Best Local Similarity: 30.56% Mismatches: 20
Query Match: 13.09% Indels: 17
Gaps: 4

US-09-801-115B-2 (1-99) x US-08-061-092A-2 (1-720)

QY 28 ILeIeAsnSerLeuValThrThrValPheMetLeuIleValSerValLeu----- 44
Db 684 GTAGTACATAGCATATGACTATAGTATAGAGCAGCATATAGACGCAGT 625
QY 45 AlaLeuIleProGluThrThrThrLeuThrValGly-----GlyGlyValPheAlaLeu 62
Db 624 GTCCTCAGATGTGAGCTGTGAGCTGAGTGAAGTGAAGCGCGGTGAGGA----- 577
QY 63 ValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLys----- 78
Db 576 -----TGCTCTGCTGTATACTGCGCTTGCGCTGGAATTTGGGTGATATACAGTATT 523
QY 79 -----LeuLeuPheAsnProSerGlyProTyrGln 88
Db 522 ACCATTCTCAGATGATGATCATTCATTCATTCCAG 487
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: January 31, 2004, 02:59:32 ; Search time 247 Seconds

(without alignments)
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Title: US-09-801-115b-2

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Delop 6.0 , Delext 7.0

Searched: 2552756 segs, 1349719017 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALLFN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
1	508	100.0	413	20	AAK97873	Human secreted pro
2	508	100.0	439	24	ABK36006	CDNA sequence #397
3	508	100.0	504	19	AAV59598	Human secreted pro
4	508	100.0	504	24	ABK37585	Human CDNA #1 for
5	508	100.0	506	19	AAV59746	Human secreted pro
6	508	100.0	506	24	ABK37339	Human CDNA #2 for
7	508	100.0	515	22	AAK64710	Human secreted pro
8	508	100.0	515	22	AAK64712	CDNA encoding huma
9	508	100.0	534	22	AAK38006	UCK-1 nucleotide s
10	508	100.0	538	22	AAK98515	Human EST-derived
11	508	100.0	538	22	AAK98548	Human EST-derived
12	508	100.0	558	22	AAH34835	Human colon cancer
13	508	100.0	655	22	AAK44932	CDNA encoding nove
14	504	99.2	297	21	AAA15919	Human protein clon
15	504	99.2	467	21	AAA15929	Human protein clon
16	489	96.3	500	20	AAK97826	Human secreted pro
17	471.5	92.8	459	21	AAK38007	UCK-2 nucleotide s
18	471.5	92.8	637	21	AAZ56747	Human Transmembran
19	471.5	92.8	663	20	AAZ34051	Human PRO772 nucle
20	471.5	92.8	663	21	AAK78498	Human PRO772 (UNQ4
21	471.5	92.8	663	21	AAK58238	Human PRO772 nucle
22	471.5	92.8	663	25	ABK92423	CDNA encoding huma
23	471.5	92.8	669	21	AAK87771	Human secreted pro
24	471.5	92.8	669	22	AAK64053	CDNA encoding huma
25	471.5	92.8	670	24	ABK90366	Human polynucleoti
26	471.5	92.8	908	22	AAK44933	CDNA encoding nove
27	467.5	92.0	638	24	ABK35884	CDNA sequence #275
28	461	90.7	415	21	AAK00147	Human secreted pro
29	357	70.3	392	21	AAK16090	Human colon cancer
30	339.5	66.8	363	21	AAK38009	UCK-4 nucleotide s
31	339.5	66.8	566	22	AAK45120	CDNA encoding nove
32	339.5	66.8	566	22	AAK45121	CDNA encoding nove
33	331	65.2	204	21	AAK38008	UCK-3 nucleotide s
34	323	63.6	321	20	AAK97651	Extended human sec
35	318.5	62.7	495	20	AAZ34052	Human EST DNA43509
36	318.5	62.7	495	21	AAK78499	Human EST DNA43509
37	318.5	62.7	495	22	AAK93358	CDNA encoding SRT
38	318.5	62.7	495	25	ABK92424	Human secreted pro
39	317	62.4	354	20	AAK41509	Human secreted pro
40	294	57.9	379	21	AAK41512	Human secreted exp
41	257.5	50.7	465	22	ABK09082	Human Transmembran
42	245	48.2	207	24	ABK94246	Gene #744 used to
43	245	48.2	207	24	ABK62782	Breast cancer rela
44	245	48.2	207	24	ABK62959	Breast cancer rela
45	245	48.2	207	24	ABK63180	Breast cancer rela

ALIGNMENTS

RESULT 1
AAK97873
ID AAK97873 standard; CDNA, 413 BP.
XX
XX AAK97873;
XX
XX 23-SEP-1999 (first entry)
XX
XX Human secreted protein encoding CDNA #61.
XX
XX Secreted protein; human; cytosolic; osteopathic; forensic;
XX
XX diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX
XX Homo sapiens.
XX
XX WO925825-A2.
XX

PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-IB01862.
XX
PR 04-SEP-1998; 98US-0099273.
PR 13-NOV-1997; 97US-0066677.
PR 17-DEC-1997; 97US-0069957.
PR 09-FEB-1998; 98US-0074121.
PR 13-APR-1998; 98US-0081563.
PR 10-AUG-1998; 98US-0096116.
XX
PA (GEMT) GENSET.
XX
PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
DR WPI; 1999-347472/29.
DR P-PSDB; AAY36189.
XX
XX Extended cDNAs encoding secreted proteins
PS Claim 1; Page 261; 307pp; English.
XX
CC AAX97813-X97906 represent extended cDNA's which encode novel human
CC secreted proteins (see AAY36129-136222) and which have cytostatic,
CC thrombotic and osteopathic activity. The extended cDNAs can be used
CC to express secreted proteins or parts of them or to obtain antibodies
CC capable of binding to the secreted proteins. They may also be used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC Uses also include design of expression vectors and secretion vectors.
XX
SQ Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;
XX
Alignment Scores:
Pred. No.: 5,46e-58 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-801-115B-2 (1-99) x AAX97873 (1-413)
QY 1 MetAspAsnValGlnProLysIleuYshIstArgProPheCysPheSerValIySGlyHis 20
Db 46 ATGGATTAACGTCGACCGCAAAATTAACAATCGCCCTTCTCTCAGTGTGAAGCCAC 105
QY 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 106 GTGAAGATGCTGCGCTGGATATTATCACTCACTGTACACAGATATTATGCTCATC 165
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrIleuThrValGlyGlyValPhe 60
Db 166 GTATCTGTGTGGACATGATACAGAAACCAACATTTGACGTGGAGGGGTGTTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIYrArgIySLeuLeu 80
Db 226 GCACCTTGACAGACAGATATGCTGCTGCCAGCGGGGCCCTTATTACCGGAAGCTTCTG 285
QY 81 PheAsnProSerGlyProTyrglnIyLeuProValHisGlyIySLeuValIleu 99
Db 286 TTCAATCCACGCGGTCTTACCAAGAAAGCGCTGTGATGATAAAAAAGAGTTTGG 342
RESULT 2
ABK36006
ID ABK36006 standard; cDNA; 439 BP.
XX
AC ABK36006;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA sequence #397 encoding novel human secreted protein.
XX
KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;

KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; allergic condition; neurodegenerative disorder;
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
KW tumour; cancer; hepatotropic; immunosuppressive; antineumatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200177289-A2.
XX
PD 18-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US10232.
XX
PR 06-APR-2000; 2000US-195605P.
XX
PA (GEMT) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Werberg D, Treacy M, Agostino WJ, Bowman MR, Spaulding V, Wong GG;
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX
DR WPI; 2002-179322/23.
XX
PT Six hundred and twenty three polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for
PT treating immune deficiencies and disorders such as autoimmune disorders
PT
PS Claim 1; Page 296-297; 393pp; English.
XX
XX The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),
CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.
CC haemophilia), and tumours. The polynucleotide sequences of the
CC invention are also useful in gene therapy. ABK3610-ABK36232 represent
CC the cDNA sequences of the invention that encode for novel human
CC secreted proteins.
XX
SQ Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;
XX
Alignment Scores:
Pred. No.: 5,93e-58 Length: 439
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-801-115B-2 (1-99) x ABK36006 (1-439)
QY 1 MetAspAsnValGlnProLysIleuYshIstArgProPheCysPheSerValIySGlyHis 20
Db 81 ATGGATTAACGTCGACCGCAAAATTAACAATCGCCCTTCTCTCAGTGTGAAGCCAC 140
QY 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 141 GTGAAGATGCTGCGCTGGATATTATCACTCACTGTACACAGATATTATGCTCATC 200
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrIleuThrValGlyGlyValPhe 60
Db 201 GTATCTGTGTGGACATGATACAGAAACCAACATTTGACGTGGAGGGGTGTTT 260
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIYrArgIySLeuLeu 80

PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1, Page 320, 721pp; English.
XX

CC This sequence represents a nucleic acid molecule designated Gene 88 from
CC the human cDNA clone HUVAV32 (deposited as clone ATCC 97901 and ATCC
CC 209047) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
CC the fused protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological conditions
CC can be diagnosed by determining the amount of the new polypeptides in a
CC sample or by determining the presence of mutations in the new

CC polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV59511 for described uses).

CC
XX
SQ Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;

Alignment Scores:

Pred. No.: 7.15e-58 Length: 504
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 19 Gaps: 0

US-09-801-115B-2 (1-99) x AAV59598 (1-504)

QY 1 MetaspasnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20

Db 131 ATGATATACGCGACGCGCAAAATAAACATGCGCCCTTCTGCTCAAGTGAAAGGCCAC 190

QY 21 ValIysMetLeuArgLeuAspIleIleasnSerLeuValThrValPheMetLeuIle 40

Db 191 GTGAAGATGCTGCGCGCTGATATTATCACTACGTGTAACACAGTATTCATCTCATC 250

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValIleGlyGlyValPhe 60

Db 251 GTACTGTGTGGACGATGATACCAAGAAACCAACATTGACAGTGGCGGGGCTTT 310

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspIleAlaLeuIleTyrArgIleLeu 80

Db 311 GCACTTGACAGCAGATGCTGCTTCCGACCGGGCCCTTATTACCGAAGCTTCTG 370

QY 81 PheAsnProSerGlyProTyrGlnLysPheProValHisGluLysGluValLeu 99

Db 371 TTCATCCGACGGCTCTTACCAAGAAAGCTGTCATGAAAAAAGAGTTTG 427

QY 371 TTCATCCGACGGCTCTTACCAAGAAAGCTGTCATGAAAAAAGAGTTTG 427

RESULT 4
ABST73585
ID ABST73585 standard; cDNA; 504 BP.

AC ABST73585;

DT 15-JAN-2003 (first entry)

DE Human cDNA #1 for novel secreted protein gene 88.

XX Human; sex; gene; secreted protein; autoimmune disease; chemotaxis;

KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;

KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;

KW cerebrovascular disorder; cerebral ischaemia; angiodysplasia; sunburn;

KW nervous system disorders; Alzheimer's disease; infection;

KW ocular disorder; corneal infection; wound healing; tissue regeneration;

KW epithelial cell proliferation; organ transplantation; food additive;

XX preservative; nutritional.
XX Homo sapiens.
OS
XX

PN US6420526-B1.

XX 16-JUL-2002.

XX 08-SEP-1998;

XX 98US-0149476.

XX 97US-038621P.

XX 97US-040161P.

XX 97US-040162P.

XX 97US-040163P.

XX 97US-040333P.

XX 97US-040334P.

XX 97US-040336P.

XX 97US-040626P.

XX 97US-043311P.

XX 97US-043312P.

XX 97US-043313P.

XX 97US-043314P.

XX 97US-043315P.

XX 97US-043568P.

XX 97US-043569P.

XX 97US-043578P.

XX 97US-043580P.

XX 97US-043692P.

XX 97US-043670P.

XX 97US-043671P.

XX 97US-043672P.

XX 97US-043674P.

XX 97US-047492P.

XX 97US-047500P.

XX 97US-047501P.

XX 97US-047502P.

XX 97US-047503P.

XX 97US-047581P.

XX 97US-047582P.

XX 97US-047583P.

XX 97US-047584P.

XX 97US-047585P.

XX 97US-047586P.

XX 97US-047587P.

XX 97US-047588P.

PR 22-AUG-1997; 97US-056662P.
PR 22-AUG-1997; 97US-056664P.
PR 22-AUG-1997; 97US-056845P.
PR 22-AUG-1997; 97US-056862P.
PR 22-AUG-1997; 97US-056864P.
PR 22-AUG-1997; 97US-056872P.
PR 22-AUG-1997; 97US-056874P.
PR 22-AUG-1997; 97US-056875P.
PR 22-AUG-1997; 97US-056876P.
PR 22-AUG-1997; 97US-056877P.
PR 22-AUG-1997; 97US-056878P.
PR 22-AUG-1997; 97US-056879P.
PR 22-AUG-1997; 97US-056880P.
PR 22-AUG-1997; 97US-056881P.
PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
PR 22-AUG-1997; 97US-056888P.
PR 22-AUG-1997; 97US-056889P.
PR 22-AUG-1997; 97US-056892P.
PR 22-AUG-1997; 97US-056893P.
PR 22-AUG-1997; 97US-056903P.
PR 22-AUG-1997; 97US-056908P.
PR 22-AUG-1997; 97US-056909P.
PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057616P.
PR 05-SEP-1997; 97US-057650P.
PR 05-SEP-1997; 97US-057669P.
PR 12-SEP-1997; 97US-058785P.
PR 02-OCT-1997; 97US-061060P.
PR 06-MAR-1998; 98MO-US04493.

(HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarek DR;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrite AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX
DR MPI; 2002-634796/68.
DR P-SDB; ABG95267.
XX
PT New isolated human secreted protein for diagnosing, preventing,
PT treating or ameliorating medical conditions and used as a food additive
PT or preservative -
XX
XX
PS Example 1; SEQ ID No 98; 129pp; English.
XX
XX The invention relates to an isolated protein that is one of 186 human
XX secreted proteins, given in the specification, encoded by one of
XX 309 cDNA sequences also given in the specification. The protein is used
XX in a pharmaceutical composition used to prevent, treat or ameliorate a
XX medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
XX dogs, chickens or sheep. Disorders which are diagnosed or treated include
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease,
XX infections caused by bacteria, viruses and fungi and ocular disorders
XX e.g. corneal infection. The polypeptides can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin aging due to
XX sunburn, to maintain organs before transplantation, for supporting cell
XX culture of primary tissues, to regenerate tissues and in chemotaxis. The
XX polypeptides can also be used as a food additive or preservative to
XX increase or decrease storage capabilities, fat content, lipid, protein,
XX carbohydrate, vitamins, minerals, cofactors and other nutritional
XX components. The present sequence represents a cDNA derived from a
XX gene encoding one of the novel human secreted proteins of the invention.
XX Note: This sequence did not form part of the printed specification,
XX but was obtained in electronic format directly from USPRO at

CC seqdata.uspto.gov/sequence.html?docID=6420526B1.
XX
XX Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;

Alignment Scores:
Pred. No.: 7 15e-58 Length: 504
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-801-115B-2 (1-99) x ABG73585 (1-504)

QY 1 MetaspasnValGlnProlysilLeuysHisArgProPheCysPheSerValIlysgIyHis 20
DB 131 ATGGATTAACGTGACGCCGAATAAATTAACATCCCTTGTGCTTCACTGTAAGGCCAC 190

QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
DB 191 GTGAAGATGCTGCGGCTGGATTTATCACTCACTGTGAACAACAGTATTCATGCTCACC 250

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAlpe 60
DB 251 GATATCTGTGTGGCACTGATACCAAGAACACACAATTACAGTTGTGAGGGGGTGT 310

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgIysLeuLeu 80
DB 311 GCACCTGTGACACAGCATATGCTGTCTTCCGACGGGGCCCTTATTTACCGGAAGCTTCTG 370

QY 81 PheAsnProSerGlyProTyrGlnIlylProValHisGluIlylValValLeu 99
DB 371 TTCATATCCACGCGGTCTTACCAAGAAAAGCCTGTGCATGAAGAAAAAGAGTTTG 427

RESULT 5
AAVS9746
ID AAVS9746 standard; DNA; 506 BP.
XX
XX
AC AAVS9746;
XX
XX
DT 19-JUN-1999 (first entry)
XX
XX
DE Human secreted protein gene 88 clone HAAUV32.
XX
XX
KM Human; secreted protein; fusion protein; gene therapy; protein therapy;
KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KM developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KM inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9839448-A2.
XX
XX
PD 11-SEP-1998.
XX
XX
PF 06-MAR-1998; 98MO-US04493.
XX
XX
PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.

PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047619.
PR 23-MAY-1997; 97US-0047632.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056633.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.

PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056899.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
DR WPI; 1998-506364/43.
DR P-PSDB; AAW74961.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1, Page 472; 721pp, English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 88 from
CC the human cDNA clone HAUW32 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
CC the fused protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV59511 for described uses).
XX
XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;
SQ
Alignment Scores:
Pred. No.: 7,19e-58 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-801-115B-2 (1-99) x AAV59746 (1-506)
QY 1 MetAspAsnValAlaInProLySIIeLySHIAzProPheCySPheserValLySgIyHis 20
Db 117 ATGAGTAACTGCGACGCGAAATTAACATCGCCCTTCGCTTCAGTGGAAGGCCAC 176
QY 21 ValLyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 177 GTGAAGATGCTGGCGGTATTAATCACTCACTGTAACAACAGATATCATGCTCATC 236
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValSgIyGlyValPhe 60
Db 237 GTATCTGTGTGGCACTGATACCAAGAACACAACTGACATGTGTGGAGGGGCTTT 296
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLySLeuLeu 80

DB 297 GCACCTGTGACAGACGATAGCTGTCTTGCCGACGGGCGCCTTAATTACCGGAAGCTTCTG 356
Qy 81 PheasnProserGlyProTyrGlnTylsLysProValHisGlnTylsLysGluValIleu 99
DB 357 TTCAATCCGACGGCTCTTCTTACGAAAAAGCCTGTGTGATATAAAAAAGAAAGTTTTC 413
RESULT 6
ID ABS73739 standard; cDNA; 506 BP.
XX ABS73739;
AC ABS73739;
XX
XX 15-JAN-2003 (first entry)
DE Human cDNA #2 for novel secreted protein gene 88.
XX
XX
XX Human; as; gene; secreted protein; autoimmune disease; chemotaxis;
KW Rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
XX Homo sapiens.
XX
XX US6420526-B1.
XX
XX 16-JUL-2002.
XX
XX 08-SEP-1998; 98US-0149476.
XX
PR 07-MAR-1997; 97US-038621P.
PR 07-MAR-1997; 97US-040161P.
PR 07-MAR-1997; 97US-040162P.
PR 07-MAR-1997; 97US-040163P.
PR 07-MAR-1997; 97US-040333P.
PR 07-MAR-1997; 97US-040334P.
PR 07-MAR-1997; 97US-040336P.
PR 07-MAR-1997; 97US-040626P.
PR 11-APR-1997; 97US-043311P.
PR 11-APR-1997; 97US-043312P.
PR 11-APR-1997; 97US-043313P.
PR 11-APR-1997; 97US-043315P.
PR 11-APR-1997; 97US-043568P.
PR 11-APR-1997; 97US-043569P.
PR 11-APR-1997; 97US-043576P.
PR 11-APR-1997; 97US-043578P.
PR 11-APR-1997; 97US-043580P.
PR 11-APR-1997; 97US-043669P.
PR 11-APR-1997; 97US-043670P.
PR 11-APR-1997; 97US-043671P.
PR 11-APR-1997; 97US-043672P.
PR 11-APR-1997; 97US-043674P.
PR 23-MAY-1997; 97US-047492P.
PR 23-MAY-1997; 97US-047500P.
PR 23-MAY-1997; 97US-047501P.
PR 23-MAY-1997; 97US-047502P.
PR 23-MAY-1997; 97US-047503P.
PR 23-MAY-1997; 97US-047581P.
PR 23-MAY-1997; 97US-047582P.
PR 23-MAY-1997; 97US-047583P.
PR 23-MAY-1997; 97US-047584P.
PR 23-MAY-1997; 97US-047585P.
PR 23-MAY-1997; 97US-047586P.
PR 23-MAY-1997; 97US-047587P.
PR 23-MAY-1997; 97US-047588P.
PR 23-MAY-1997; 97US-047589P.
PR 23-MAY-1997; 97US-047590P.
PR 23-MAY-1997; 97US-047592P.
PR 23-MAY-1997; 97US-047593P.

PR 23-MAY-1997; 97US-047594P.
PR 23-MAY-1997; 97US-047595P.
PR 23-MAY-1997; 97US-047596P.
PR 23-MAY-1997; 97US-047597P.
PR 23-MAY-1997; 97US-047598P.
PR 23-MAY-1997; 97US-047599P.
PR 23-MAY-1997; 97US-047600P.
PR 23-MAY-1997; 97US-047601P.
PR 23-MAY-1997; 97US-047612P.
PR 23-MAY-1997; 97US-047613P.
PR 23-MAY-1997; 97US-047614P.
PR 23-MAY-1997; 97US-047615P.
PR 23-MAY-1997; 97US-047617P.
PR 23-MAY-1997; 97US-047618P.
PR 23-MAY-1997; 97US-047632P.
PR 23-MAY-1997; 97US-047633P.
PR 06-JUN-1997; 97US-048964P.
PR 06-JUN-1997; 97US-048974P.
PR 13-JUN-1997; 97US-049610P.
PR 08-JUL-1997; 97US-051926P.
PR 16-JUL-1997; 97US-052874P.
PR 18-AUG-1997; 97US-055724P.
PR 22-AUG-1997; 97US-056630P.
PR 22-AUG-1997; 97US-056631P.
PR 22-AUG-1997; 97US-056632P.
PR 22-AUG-1997; 97US-056636P.
PR 22-AUG-1997; 97US-056637P.
PR 22-AUG-1997; 97US-056662P.
PR 22-AUG-1997; 97US-056664P.
PR 22-AUG-1997; 97US-056845P.
PR 22-AUG-1997; 97US-056846P.
PR 22-AUG-1997; 97US-056872P.
PR 22-AUG-1997; 97US-056874P.
PR 22-AUG-1997; 97US-056875P.
PR 22-AUG-1997; 97US-056876P.
PR 22-AUG-1997; 97US-056877P.
PR 22-AUG-1997; 97US-056878P.
PR 22-AUG-1997; 97US-056879P.
PR 22-AUG-1997; 97US-056880P.
PR 22-AUG-1997; 97US-056881P.
PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
PR 22-AUG-1997; 97US-056888P.
PR 22-AUG-1997; 97US-056889P.
PR 22-AUG-1997; 97US-056892P.
PR 22-AUG-1997; 97US-056893P.
PR 22-AUG-1997; 97US-056894P.
PR 22-AUG-1997; 97US-056903P.
PR 22-AUG-1997; 97US-056908P.
PR 22-AUG-1997; 97US-056909P.
PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057761P.
PR 05-SEP-1997; 97US-057650P.
PR 05-SEP-1997; 97US-057669P.
PR 12-SEP-1997; 97US-057852P.
PR 02-OCT-1997; 97US-061060P.
PR 06-MAR-1998; 98WO-US04493.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrle AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI, 2002-634796/68.
DR P-PSDB; ABG95421.
XX

New isolated human secreted protein for diagnosing, preventing,

PT treating or ameliorating medical conditions and used as a food additive
PT or preservative -

PS Example 1; SEQ ID No 252; 129pp; English.

CC The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of
CC 309 cDNA sequences also given in the specification. The protein is used
CC in a pharmaceutical composition used to prevent, treat or ameliorate a
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents a cDNA derived from a
CC gene encoding one of the novel human secreted proteins of the invention.
CC Note: This sequence did not form part of the printed specification,
CC but was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=6420526b1.

XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;

Alignment Scores:

Pred. No.:	7.19e-58	Length:	506
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-801-115B-2 (1-99) x ABB573739 (1-506)

QY 1 MetAspAsnValGlnProLysIleLeuHisArgProPheCysPheSerValIleGlyHis 20
DB 117 ATGATTAACGTCGACCGCAAAATTAACATGCCCCCTTCTGCTCAGTGTAAGGCCAC 176
QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 177 GTGAAGATGTCGGCGCTGATATTATCACTCACTGGTAACAACAAGATATGCTCATC 236
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 237 GTATCTGTGTTGGACATGATACAGAAACCAACATTTGATGGAGGGGTGTTT 296
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
DB 297 GCACCTGTGAACAGATATGCTGCTTGGCCGACGGGGCCCTTATTATCCGGAAGCTTCTG 356
QY 81 PheAsnProSerGlyProTyrGlnIleLysPheProValHisGluLysGluValLeu 99
DB 357 TTCAATCCACAGCGGTCTTACCAAAAAAGCTGTGATGAAAAAAGAGTTTG 413

RESULT 7

AAA87730 standard; cDNA; 515 BP.

XX AAA87730;

XX 28-NOV-2000 (first entry)

DE Human secreted protein encoding cDNA SEQ ID #29.

XX Human; secreted protein; forensic procedure; gene therapy;
KM chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;

KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
KW mitochondrialcytopathy; diabetes; atherosclerosis; Alzheimer's disease;
KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KW septic shock; impotence; ss.

XX Homo sapiens.

XX WO200037491-A2.

XX 29-JUN-2000.

XX 20-DEC-1999; 99WO-IB02058.

XX 22-DEC-1998; 98US-0113686.

XX 25-JUN-1999; 99US-0141032.

XX (GEST) GENSET.

XX Bougueleret L, Dumas J, Duclert A;

XX WPI; 2000-442637/38.

XX P-PSDB; AAB25768.

XX Polynucleotides and polypeptides encoding proteins with signal
XX peptides, useful in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures -

XX Claim 1; Page 169-170; 306pp; English.

CC This sequence represents human cDNA encoding a secreted protein. The
CC invention relates to sequences AAA87725-A87774 which encode human
CC secreted proteins AAB25763-B25812. The proteins include signal peptides.
CC Included in the invention are a host cell containing one of the cDNA
CC sequences, and a purified antibody capable of binding to one of the
CC secreted proteins. Also contained in the invention are methods for
CC storing the sequence data on a computer system, and a method for
CC identifying features of the cDNA sequences using a computer programme.
CC The cDNAs are useful for expressing secreted proteins or fragments to
CC obtain antibodies capable of specifically binding to the secreted
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
CC therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondrialcytopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence.

XX Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Alignment Scores:

Pred. No.:	7.36e-58	Length:	515
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-801-115B-2 (1-99) x AAA87730 (1-515)

QY 1 MetAspAsnValGlnProLysIleLeuHisArgProPheCysPheSerValIleGlyHis 20

DB 144 ATGATTAACGTCGACCGCAAAATTAACATGCCCCCTTCTGCTCAGTGTAAGGCCAC 203

QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

DB 204 GTGAAGATGTCGGCGCTGATATTATCACTCACTGGTAACAACAAGATATGCTCATC 263

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

DB 264 GTATCTGTGTTGGACATGATACAGAAACCAACATTTGATGGAGGGGTGTTT 323

```
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 324 GCACCTGTGACAGACAGATATGCTGTGCGACGGGGCCCTTATTACCGGAAGCTTCG 383
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
DB 384 TTCAAATCCAGCGGCTCTTACGAGAAAAGCCCTGTGCATGAAAAAAGAGTTTGG 440

RESULT 8
AAF64012
ID AAF64012 standard; cDNA; 515 BP.
AC AAF64012;
DT 05-APR-2001 (first entry)
DE cDNA encoding human secreted protein #13.
KW Secreted protein; prevention; treatment; diagnosis; disease;
XX infection; ds.
OS Homo sapiens.
PN MO200100806-A2.
PD 04-JAN-2001.
PF 21-JUN-2000; 2000MO-IB00951.
XX
XX 25-JUN-1999; 99US-0141032.
PR 21-DEC-1999; 99US-0469099.
XX
XX (GEST ) GENSET.
PI Dumas Maline Edwards J, Bougueleret L, Joberet S;
DR WPI; 2001-071487/08.
XX
XX 49 Secreted proteins and the nucleic acids encoding them, useful in
PT gene therapy and for detecting similar sequences in samples -
XX
XX Claim 1; Page 225; 307pp; English.
XX
CC The present invention relates to 49 Secreted proteins and the cDNAs
CC encoding them. The protein and nucleic acids may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate protein expression.
XX
SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Alignment Scores:
Pred. No.: 7.36e-58 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAF64012 (1-515)
QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 144 ATGGATTAACGTGACGCCGAAATTAACATCGCCCTTCTGCTTCACTGTAAGGCCAC 203
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 204 GTGAAGATGCTGGCGCTGGATATATATCACTGATGAACAACAGATTATCATGCTCATC 263
QY 41 ValSerValLeuAlaLeuIleProGlnThrThrThrThrLeuThrValGlyGlyValPhe 60
DB 264 GTATCTGTGTTGGCATGATACCAAGAAACCAACACATTCAGTTGATGGAGGGGTGTTT 323
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QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 324 GCACCTGTGACAGACAGATATGCTGTGCGACGGGGCCCTTATTACCGGAAGCTTCG 383
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
DB 384 TTCAAATCCAGCGGCTCTTACGAGAAAAGCCCTGTGCATGAAAAAAGAGTTTGG 440

RESULT 9
AAA38006
ID AAA38006 standard; cDNA; 534 BP.
AC AAA38006;
DT 22-AUG-2000 (first entry)
DE UCK-1 nucleotide sequence.
XX
XX UCK-1; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
KW radiotherapy; chemotherapy; human; ss.
XX
OS Homo sapiens.
PN CN1244584-A.
PD 16-FEB-2000.
PF 14-MAY-1999; 99CN-0107284.
XX
XX 14-MAY-1999; 99CN-0107284.
PR 14-MAY-1999; 99CN-0107284.
XX
XX (UYBE-) UNIV BEIJING MEDICAL.
PI Ma D, Han W, Zhang Y;
DR WPI; 2000-388170/34.
XX
XX P-PSDB; AAY98142.
XX
XX Chemotactic factor useful for treatment and diagnosis of immunocyte
PT disorders - has immunocyte chemotactic stimulating factor
XX
XX Example 4; Fig 1; 31pp; Chinese.
XX
CC This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis
CC factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis
CC activity and a haemopoiesis stimulating effect. The invention relates to
CC UCK proteins, their encoding nucleotide sequences and antibodies and
CC antagonists against the proteins. The nucleotide and protein sequences
CC are useful for the preparation of a composition for the diagnosis and
CC treatment of diseases associated with abnormal immunocyte function and
CC low haemopoiesis function caused by radiotherapy and chemotherapy used to
CC treat tumours and other diseases.
XX
SQ Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;

Alignment Scores:
Pred. No.: 7.73e-58 Length: 534
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-801-115B-2 (1-99) x AAA38006 (1-534)
QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 152 ATGGATTAACGTGACGCCGAAATTAACATCGCCCTTCTGCTTCACTGTAAGGCCAC 211
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 212 GTGAAGATGCTGGCGCTGGATATATATCACTGATGAACAACAGATTATCATGCTCATC 271
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Qy 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 272 GTATCTGTGTGGACGATACGAGAAACCAACATTCAGTGTGGAGGGGCTTT 331
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgGlyLeuLeu 80
Db 332 GCACCTGTGACAGACGATAGCTGTCTGGCCGACGGGGCCCTTATTATCCGAAACCTTCTG 391
Qy 81 PheAsnProSerGlyProTyrGlnIleValSerProValHisGluIleValGluValIleu 99
Db 392 TTCATCCACGCGGTCTTACCAAGAAAGCCCTGTGATGAAAAAGAAAGTTTGG 448

RESULT 10
AAH98515/c
ID AAH98515 standard; cDNA; 538 BP.
XX
AC AAH98515;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 372.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dormanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR P-PSDB; AAM23856.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 451; 1275bp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

Alignment Scores:
Pred. No.: 7.81e-58 Length: 538
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAH98515 (1-538)
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```
Qy 1 MetAspAsnValGlnProIleLeuIleValArgProPheCysPheSerValIleGlyHis 20
Db 366 ATGATTAAGCTGACGACGCGAAATATAAATATGCGCCCTTCTGCTTCACTGTAAGAAAGCCAC 307
Qy 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 306 GTGAAATGATGTGGCTGGATATTAACAATCACTAGTAAACAACATATTCATGCTTCATC 247
Qy 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 246 GTATCTGTGTGGACCTGATACGAGAAACCAACATTCAGTGTGGAGGGGCTTT 187
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgGlyLeuLeu 80
Db 186 GCACCTGTGACAGACGATAGCTGTCTGGCCGACGGGGCCCTTATTATCCGAAAGCTTCTG 127
Qy 81 PheAsnProSerGlyProTyrGlnIleValSerProValHisGluIleValGluValIleu 99
Db 126 TTCATCCACGCGGTCTTACCAAGAAAGCCCTGTGATGAAAAAGAAAGTTTGG 70

RESULT 11
AAH98548/c
ID AAH98548 standard; cDNA; 538 BP.
XX
AC AAH98548;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 405.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dormanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR P-PSDB; AAM23889.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 467; 1275bp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;
```


Alignment Scores:
Pred. No.: 7,81e-58 Length: 538
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAH98548 (1-538)

QY 1 MetAspAsnValGlnProIlySilIeLysHisArgProPheCysPheSerValIySgIyHis 20
Db 366 ATGGATTAACGTGACGCGGAAATTAACATCGCCCTTCCTTCAGTGGAAGGCAC 307
QY 21 ValIySerMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 306 GTGAAGATGCTGGCGCTGGATATTAATCACTGTTAACAACAGATTCAAGCTCATT 247
QY 41 ValSerValIleuAlaIleuIleProGluThrThrThrIleuValGlyGlyValPhe 60
Db 246 GTATCTGTGTGGACATGATACCAAGAACCAACATTGACGTTGGTGGAGGGGTGTTT 187
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyraGlyLeu 80
Db 186 GCACCTGTGACACAGATGCTGTCTTGGCCGACGGGCGCTTATTATCCGGAAGCTTCTG 127
QY 81 PheAsnProSerGlyProTyrgInIyLysProValHisGluIySgIyValIleu 99
Db 126 TTCATATCCACGGCGCTCTTACAGAAAAGCCTGTGCATGAAAAAGAGTTTGG 70

RESULT 12
AAH34835
ID AAH34835 standard; cDNA; 558 BP.
XX
AC AAH34835;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX
OS Colorectal carcinoma; ss.
XX
PN Homo sapiens.
XX
MO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000MO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
XX
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI, 2001-235357/24.
XX
P-PSDB; AAG75430.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX
useful for preventing, diagnosing and/or treating colorectal cancers -
XX
Claim 1; Page 3428; 9803pp; English.
XX
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX
cancer-associated nucleic acid molecules (N) and proteins (P), where
XX
the proteins are collectively known as colon cancer antigens. The colon
XX
cancer antigens have cytostatic activity and can be used in gene
XX
therapy and vaccine production. N and P may be used in the prevention,
XX
diagnosis and treatment of diseases associated with inappropriate P
XX
expression. For example, N and P may be used to treat disorders

CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;

Alignment Scores:
Pred. No.: 8,21e-58 Length: 558
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAH34835 (1-558)

QY 1 MetAspAsnValGlnProIlySilIeLysHisArgProPheCysPheSerValIySgIyHis 20
Db 147 ATGGATTAACGTGACGCGGAAATTAACATCGCCCTTCCTTCAGTGGAAGGCAC 206
QY 21 ValIySerMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 207 GTGAAGATGCTGGCGCTGGATATTAATCACTGTTAACAACAGATTCAAGCTCATT 266
QY 41 ValSerValIleuAlaIleuIleProGluThrThrThrIleuValGlyGlyValPhe 60
Db 267 GTATCTGTGTGGACATGATACCAAGAACCAACATTGACGTTGGTGGAGGGGTGTTT 326
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyraGlyLeu 80
Db 327 GCACCTGTGACACAGATGCTGTCTTGGCCGACGGGCGCTTATTATCCGGAAGCTTCTG 386
QY 81 PheAsnProSerGlyProTyrgInIyLysProValHisGluIySgIyValIleu 99
Db 387 TTCATATCCACGGCGCTCTTACAGAAAAGCCTGTGCATGAAAAAGAGTTTGG 443

RESULT 13
AAS44932
ID AAS44932 standard; cDNA; 655 BP.
XX
AC AAS44932;
XX
DT 18-DEC-2001 (first entry)
XX
DE cDNA encoding novel human secretory protein, Seq ID No 13.
XX
KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX
KW ischemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
XX
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
XX
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
XX
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
XX
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
XX
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
XX
fertility; analgesic; pain; antigen; ss.
XX
OS Homo sapiens.
XX
PN MO200166689-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001MO-US04942.
XX

CC infectious diseases caused by viral, bacterial, fungal or other
 CC infections. The protein is also used for treating autoimmune disorders
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
 CC arthritis. It is also useful in the treatment of allergic reactions and
 CC conditions such as asthma, and in immune suppression after organ
 CC transplantation. The protein is useful in regulation of haematopoiesis
 CC and consequently in the treatment of myeloid or lymphoid cell
 CC deficiencies. It is also used in compositions for tissue growth or
 CC regeneration. The protein is also used in the treatment of osteoporosis
 CC or osteoarthritis and in the treatment of periodontal disease and other
 CC tooth repair processes. The protein is used in the treatment of nervous
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and
 CC Huntington's disease. They are useful for protection or regeneration and
 CC treatment of lung or liver fibrosis, reperfusion injury in various
 CC tissues, and conditions resulting from systemic cytokine damage. They are
 CC also used for promoting or inhibiting tissue differentiation. They are
 CC also used as contraceptives since they exhibit activin or inhibin related
 CC activities and as a fertility inducing therapeutic. They are used for
 CC treating various coagulation disorders and in treatment and prevention of
 CC conditions resulting from coagulation activities e.g. myocardial
 CC infarction or stroke. They also acts as receptors, receptor ligands or
 CC inhibitors or agonists of receptor/ligand interactions. They are used to
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
 CC reperfusion injury, arthritis, and nephritis. They can be used to
 CC prevent tumours.

XX Sequence 297 BP: 81 A; 68 C; 72 G; 76 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	297
Score:	504.00	Matches: 98
Percent Similarity:	100.00%	Conservative: 1
Best Local Similarity:	98.99%	Mismatches: 0
Query Match:	99.21%	Indels: 0
DB:	21	Gaps: 0

US-09-801-115B-2 (1-99) x AAA15919 (1-297)

QY 1 MetAspAsnValGlnPolysIleIleValHisArgProPheCysPheSerValIleValHis 20
 Db 1 ATGATATACGTCGACGCGAAATAAACATCGCCCCCTTCCTGCTCACTGGAAAGGCGCAC 60
 QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValIlePheMetLeuIle 40
 Db 61 GTGAAGATGCTGCGCGCTGATATATATCACTGATGTAACAAGATTCATCTCATC 120
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAlaPhe 60
 Db 121 GTATCTGTGTGGCACTGATACAGAAACCAACATTCAGATTGATGGAGGGGTGTTT 180
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleIleValLeuLeu 80
 Db 181 GCACCTTGTGACAGAGATATGCTGCTGCCACGCGGCGCTTATTTCCGAAAGCTTCTG 240
 QY 81 PheAsnProSerGlyProTyrGlnIleValProValHisGluIleValValIle 99
 Db 241 TTCAATCCAGCGGTCTTACCAAGAAAGCCTTGATGATAAAAGAAAGTTTGG 297

RESULT 15

AAA15929 standard; cDNA; 467 BP.

XX AAA15929;

XX 12-JUN-2000 (first entry)

DE Human protein clone HP10357 full length coding sequence.

XX Human protein; hydrophobic domain; nutritional source; haematopoiesis;

KW cytokine production; cell proliferation; cell differentiation;

KW immune deficiency; infectious disease; autoimmune disorder; asthma;

KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;

KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;

KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy; ss.

XX Homo sapiens.

XX MO200005367-A2.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-JP03929.

XX 24-JUL-1998; 98JP-0208820.

XX 07-AUG-1998; 98JP-0224105.

XX 25-AUG-1998; 98JP-0238116.

XX 09-SEP-1998; 98JP-0254736.

XX 29-SEP-1998; 98JP-0275505.

XX (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI; 2000-182694/16.

XX P-P-SDB; AAY94861.

XX Novel human proteins having hydrophobic domains useful for treating

XX osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,

XX multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -

XX Claim 4; Page 228; 35pp; English.

XX This sequence encodes a human protein of the invention, which has

XX hydrophobic domains. The DNA sequences can be used as a probe or as a

XX genetic marker. The protein can also be used as a marker, and to identify

XX potential genetic disorders. The DNA and protein can also be used as

XX nutritional sources or supplements. The protein exhibits cytokine, cell

XX proliferation, cell differentiation activities and induces production of

XX other cytokines in certain cell populations. The protein also exhibits

XX immune stimulating or immune suppressing activity. It can be used in the

XX treatment of various immune deficiencies and disorders, and to treat

XX infectious diseases caused by viral, bacterial, fungal or other

XX infections. The protein is also used for treating autoimmune disorders

XX such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid

XX arthritis. It is also useful in the treatment of allergic reactions and

XX conditions such as asthma, and in immune suppression after organ

XX transplantation. The protein is useful in regulation of haematopoiesis

XX and consequently in the treatment of myeloid or lymphoid cell

XX deficiencies. It is also used in compositions for tissue growth or

XX regeneration. The protein is also used in the treatment of osteoporosis

XX or osteoarthritis and in the treatment of periodontal disease and other

XX tooth repair processes. The protein is used in the treatment of nervous

XX system disorders such as Alzheimer's disease, Parkinson's disease, and

XX Huntington's disease. They are useful for protection or regeneration and

XX treatment of lung or liver fibrosis, reperfusion injury in various

XX tissues, and conditions resulting from systemic cytokine damage. They are

XX also used for promoting or inhibiting tissue differentiation. They are

XX also used as contraceptives since they exhibit activin or inhibin related

XX activities and as a fertility inducing therapeutic. They are used for

XX treating various coagulation disorders and in treatment and prevention of

XX conditions resulting from coagulation activities e.g. myocardial

XX infarction or stroke. They also acts as receptors, receptor ligands or

XX inhibitors or agonists of receptor/ligand interactions. They are used to

XX treat inflammatory conditions such as septic shock, sepsis, ischaemia

XX reperfusion injury, arthritis, and nephritis. They can be used to

XX prevent tumours.

XX Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other;

XX Alignment Scores:

Pred. No.: 2.19e-57 Length: 467
Score: 504.00 Matches: 98
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.99% Mismatches: 0
Query Match: 99.21% Indels: 0
DB: 21 Gaps: 0

US-09-801-115B-2 (1-99) x AAA15929 (1-467)

OY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20
Db 114 ATGGATACGTGCACCGCAAAATATAACATGCCCCCTTCTGCTTCAGTGTGAAGGCCAC 173
OY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 174 GTGAAGATGCTGCGGCTGTGATATTATCACTCAGTACACAGATATCATGCTCATC 233
OY 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
Db 234 GTATCTGTGTGGCACTGATACCAAGAACCAACATTGACAGTGTGTGAGGGGTGTTT 293
OY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
Db 294 GCACCTGTGACAGCAGTATGCTGTTCGCAAGGGGCCCTTATTACCGAAGCTTCTG 353
OY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
Db 354 TTCAATCCACAGGCTTACACAGCAAAAGCTGTGATGAAAAAAGAAAGTTTG 410

Search completed: January 31, 2004, 04:20:24
Job time : 249 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2004, 04:09:48 ; Search time 2058 Seconds
(without alignments)
1169.166 Million cell updates/sec

Title: US-09-801-115B-2
Perfect score: 508
Sequence: 1 MDVQPKIKRPFCEVYKH.....LFNPSGPYQKPKVHEKKEVL 99

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/p/US09801115/runat.30012004.113848.7035/app_query.fasta.1.263
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=p2c -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=6 -ICPU=3
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estom.*
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17: em_gss_hum.*
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20: em_gss_vrt.*
21: em_gss_fun.*
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24: em_gss_pro.*
25: em_gss_tod.*
26: em_gss_phg.*
27: em_gss_vr1.*
28: gb_gss1.*

29: gb_gss2.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	508	100.0	AA911088	AA911088 OK67601.S
2	508	100.0	AI989739	AI989739 w0210.x
3	508	100.0	AM183193	AM183193 xj67f11.x
4	508	100.0	AA516431	AA516431 ne58a03.s
5	508	100.0	AI989747	AI989747 w021f09.x
6	508	100.0	BM553628	BM553628 AGENCOURT
7	508	100.0	AI826623	AI826623 w055d10.x
8	508	100.0	AI128804	AI128804 qas4b08.s
9	508	100.0	AA455042	AA455042 a04a07.s
10	508	100.0	AA429945	AA429945 zw67f10.s
11	508	100.0	AI078580	AI078580 cz37h05.x
12	508	100.0	AI743235	AI743235 w090a02.x
13	508	100.0	AI743235	AI743235 w090a02.x
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16	508	100.0	AI743235	AI743235 w090a02.x
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20	508	100.0	AI743235	AI743235 w090a02.x
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22	508	100.0	AI743235	AI743235 w090a02.x
23	508	100.0	AI743235	AI743235 w090a02.x
24	508	100.0	AI743235	AI743235 w090a02.x
25	508	100.0	AI743235	AI743235 w090a02.x
26	508	100.0	AI743235	AI743235 w090a02.x
27	508	100.0	AI743235	AI743235 w090a02.x
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29	508	100.0	AI743235	AI743235 w090a02.x
30	508	100.0	AI743235	AI743235 w090a02.x
31	508	100.0	AI743235	AI743235 w090a02.x
32	508	100.0	AI743235	AI743235 w090a02.x
33	508	100.0	AI743235	AI743235 w090a02.x
34	508	100.0	AI743235	AI743235 w090a02.x
35	508	100.0	AI743235	AI743235 w090a02.x
36	508	100.0	AI743235	AI743235 w090a02.x
37	508	100.0	AI743235	AI743235 w090a02.x
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39	508	100.0	AI743235	AI743235 w090a02.x
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41	508	100.0	AI743235	AI743235 w090a02.x
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44	508	100.0	AI743235	AI743235 w090a02.x
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ALIGNMENTS

RESULT 1
AA911088/c
LOCUS AA911088 386 bp mRNA linear EST 09-JUN-1998
DEFINITION OK67601.61 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519032 3'
ACCESSION AA911088
VERSION AA911088.1 GI:3050378
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 386)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/HLNLT at:
www.bio.11nl.gov/bdrip/image/image.html
Insert Length: 381 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 79.
Location/Qualifiers
1. 386
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1519032"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 113 a 87 c 81 g 105 t
ORIGIN

Alignment Scores:
Pred. No.: 2.92e-56 Length: 386
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AA911088 (1-386)

QY 1 MetApsanValGlnProlysllelyshiaArgProPhCySpheSerVallysglyhis 20
DB 357 ATGGATACGTGCGCGGAAATAAACATCGCCCTTCTGCTTCACTGTGAAGGCCAC 298

QY 21 VallysMetLeuArgleuAspIleleAsnSerleuValThrThrValPheMetleuile 40
DB 297 GTGAAAGTGTGCGCGCTGATATTATCACTGTAACACAGATTCACTGCTATC 238

QY 41 ValSerValleuAlaLeuileProgluThrThrThreuthrValglyglyValPhe 60
DB 237 GTATCTGTGTGGCACTGATACCAAGAACCAACATTGACAGTGTGAGGGGCTTT 178

QY 61 AlaleuValThralaValCysCysleuAlaaspGlyAlaLeuileTyraGlySleuLeu 80
DB 177 GCACCTGTGACAGAGTATCTGTCTGCGACGGGGCCCTTATTATCCGGAAGCTTCTG 118

QY 81 PheAsnProSerGlyProTyrglnlyslsProValHisglulyslysgluValleu 99
DB 117 TTCATCCAGCGGCTCTTACAGAAAAGCTGTGATGAAAAAAGAGTTTGG 61

RESULT 2
LOCUS AI989739 391 bp mRNA linear EST 27-OCT-1999
DEFINITION wu21e10.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone
IMAGE:2520714 3', mRNA sequence.
ACCESSION AI989739

VERSION AI989739.1 GI:5836620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 391)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through HLNLT; contact the
IMAGE Consortium (info@image.11nl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 391
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2520714"
/tissue_type="colonic mucosa from 3 patients with Crohn's
disease"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAACTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Tissue samples
provided by Dr. Brian Dieckgraefe (Washington University,
dieck@im.wustl.edu); colonic mucosa represents a range of
disease involvement from moderate to severe Crohn's
disease; samples include both perforating (fistulas) and
non-perforating samples. Library constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 113 a 90 c 81 g 107 t
ORIGIN

Alignment Scores:
Pred. No.: 2.97e-56 Length: 391
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AI989739 (1-391)

QY 1 MetApsanValGlnProlysllelyshiaArgProPhCySpheSerVallysglyhis 20
DB 358 ATGGATACGTGCGCGGAAATAAACATCGCCCTTCTGCTTCACTGTGAAGGCCAC 299

QY 21 VallysMetLeuArgleuAspIleleAsnSerleuValThrThrValPheMetleuile 40
DB 298 GTGAAAGTGTGCGCGCTGATATTATCACTGTAACACAGATTCACTGCTATC 239

QY 41 ValSerValleuAlaLeuileProgluThrThrThreuthrValglyglyValPhe 60
DB 238 GTATCTGTGTGGCACTGATACCAAGAACCAACATTGACAGTGTGAGGGGCTTT 179

QY 61 AlaleuValThralaValCysCysleuAlaaspGlyAlaLeuileTyraGlySleuLeu 80
DB 178 GCACCTGTGACAGAGTATCTGTCTGCGACGGGGCCCTTATTATCCGGAAGCTTCTG 119

QY 81 PheAsnProSerGlyProTyrglnlyslsProValHisglulyslysgluValleu 99
DB 118 TTCATCCAGCGGCTCTTACAGAAAAGCTGTGATGAAAAAAGAGTTTGG 62

RESULT 3
AW183193/c 396 bp mRNA linear EST 18-NOV-1999
LOCUS x167f11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
DEFINITION IMAGE:2662317 3', mRNA Sequence.
ACCESSION AM183193
VERSION AM183193.1 GI:6451679
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from gibco.
Location/Qualifiers
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2662317"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung BHL19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729086-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 115 a 92 c 80 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 3.01e-56 Length: 396
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x AW183193 (1-396)
QY 1 MetaspasnValGlnProlysiilelyshisargProphesCysPheSeraVallysglyhis 20
Db 359 ATGGATTAACGTGCGAGCCGAAATTAACATGCCCCCTTCTGCTTCAAGTGGAAAGGCCAC 300
QY 21 VallysmetleuargleuaspiileleasnserleuValThrThyValPheMetleuile 40
Db 299 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACAAACAGTATTCATCTCATC 240
QY 41 ValserValleualaleuileprogluThrThrThreuthrValglyglyValPhe 60
Db 239 GTACTGTGTGGACATGATCCAGAAACCAACACATTGACAGTGGTGGAGGGGCTGT 180
QY 61 AlaleuValThrAlaValCysCysleuValaspGlyAlaValleuileTyArglyLeuileu 80
Db 179 GCACTTGTGACACAGTATGCTGCTCTCCACAGGGGCCCTTATTATCCGAAAGCTCTG 120
QY 81 PheasnProserGlyProTyGlnlyslsProValHisgluTylysglyValleu 99
|||||

Db 119 TTCATCCAGCGGCTCTTACCAAGAAAGCCCTGTCATGAAAAAAGAGCTTTG 63
RESULT 4
AA516431/c 399 bp mRNA linear EST 13-AUG-1997
LOCUS AA516431
DEFINITION nes8403.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:901516 3',
mRNA sequence.
ACCESSION AA516431
VERSION AA516431.1 GI:2255955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 399)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Elise Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdip/image/image.html
Insert Length: 527 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amerham.
Location/Qualifiers
1..399
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:901516"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/clone_lib="NCI CGAP C03"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia). digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library went through one round of
normalization."
BASE COUNT 115 a 94 c 81 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 3.04e-56 Length: 399
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x AA516431 (1-399)
QY 1 MetaspasnValGlnProlysiilelyshisargProphesCysPheSeraVallysglyhis 20
Db 357 ATGGATTAACGTGCGAGCCGAAATTAACATGCCCCCTTCTGCTTCAAGTGGAAAGGCCAC 238
QY 21 VallysmetleuargleuaspiileleasnserleuValThrThyValPheMetleuile 40
Db 297 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACAAACAGTATTCATCTCATC 228
QY 41 ValserValleualaleuileprogluThrThrThreuthrValglyglyValPhe 60
Db 237 GTACTGTGTGGACATGATCCAGAAACCAACACATTGACAGTGGTGGAGGGGCTGT 178
|||||

QY 61 AAlaevAlThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLySLeuLeu 80
 Db 177 GCACCTTGACAGCAGTATGCTGCTTCCACGCGGCCCTTATTACCGGAACCTCTG 118
 QY 81 PheAsnProSerGlyProTyGlnLysLysProValHisGlyLysLysGluValLeu 99
 Db 117 TTCATCCACGCGCTTACCAAGAAAGCCGTGTCATGAAAAAAGAGTTTGG 61
 RESULT 5
 A1989747/c 402 bp mRNA linear EST 27-OCT-1999
 LOCUS wu21f09.x1 Soares Dieckgraefe.colon_NHCD Homo sapiens cDNA clone
 DEFINITION IMAGE:2520713 3', mRNA sequence.
 A1989747
 ACCESSION A1989747 GI:5836628
 VERSION A1989747.1 GI:5836628
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 402)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -400p from GIBCO.
 FEATURES
 source
 1. 402
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2520713"
 /tissue_type="colonic mucosa from 3 patients with Crohn's
 disease"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Soares_Dieckgraefe.colon_NHCD"
 /note="Organ: colon; Vector: pTV73D-Pac (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pTV73 vector. Library
 went through one round of normalization. Tissue samples
 provided by Dr. Brian Dieckgraefe (Washington University,
 dieck@wustl.edu); colonic mucosa represents a range of
 disease involvement from moderate to severe Crohn's
 disease; samples include both perforating (fistulas) and
 non-perforating samples. Library constructed by Bento
 Soares and M. Fatima Bonalho.

BASE COUNT 113 a 90 c 82 g 117 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,07e-56 Length: 402
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-801-115B-2 (1-99) x A1989747 (1-402)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
 Db 368 ATGATTAACGTCGACGCCGAAATAAATACATCGCCCTTCTGCTTCAAGTGTAAGGCCAC 309
 QY 21 ValLysMetLeuArgLysAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

Db 308 GTAAAGATGCTGGCGGTGGATATTATCACTCACTGTAACAACAGTATTCACTCATC 249
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
 Db 248 GATCTGTGTGGACATGATGCTGTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 189
 QY 61 AAlaevAlThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLySLeuLeu 80
 Db 188 GCACCTTGACAGCAGTATGCTGCTTCCACGCGGCCCTTATTACCGGAACCTCTG 129
 QY 81 PheAsnProSerGlyProTyGlnLysLysProValHisGlyLysLysGluValLeu 99
 Db 128 TTCATCCACGCGCTTACCAAGAAAGCCGTGTCATGAAAAAAGAGTTTGG 72
 RESULT 6
 BM553628 404 bp mRNA linear EST 20-FEB-2002
 LOCUS BM553628
 DEFINITION AGENCOURT_5541772 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5740478
 5', mRNA sequence.
 ACCESSION BM553628.1 GI:18792524
 VERSION BM553628.1 GI:18792524
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 404)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLAM12755 row: h column: 15
 High quality sequence stop: 403.
 FEATURES
 source
 1. 404
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5740478"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC 88"
 /note="Organ: small intestine; Vector: PCMV-SPORT6;
 Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 121 a 80 c 87 g 116 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.09e-56 Length: 404
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0
 US-09-801-115B-2 (1-99) x BM553628 (1-404)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
 Db 32 ATGATTAACGTCGACGCCGAAATAAATACATCGCCCTTCTGCTTCAAGTGTAAGGCCAC 91

Qy	21	ValiysmetLeuA	gyleuAspIleleEmserLeuValThrTrValPheMetLeuIle	40
Db	92	GTGAAGATGCTCGCGCTGGATATTTATTTACTCACTGGTAAACAAGATTTATCTCATC	151	
Qy	41	ValserValleuA	leuAleuIleProGluThrThrThreuthrValIglYglYValPhe	60
Db	152	GTATCTGTTGGCACTGATACAGAAACCAACATGACAGTTGGTGGAGGGGTGTTT	211	
Qy	61	AlAleuValThrAlaValCyeCysLeuAlaAspGlyAlaLeuIleTyArgYsLeuLeu	80	
Db	212	GCACCTTGGACGACGATATGCTGCTTCCACACGGGGCCCTTATTTTCCGGAACTTCTG	271	
Qy	81	PheAsnProSerGlyProTyGlnLysLysProValHisGluLysGluValLeu	99	
Db	272	TTCAATCCACGGCTCTTACCAAGAAAGCCTTGATGAAAGAAAGAGTTTGG	328	
RESULT 7				
LOCUS	AI826623/c			
DEFINITION	WK35410.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417395 3'			
ACCESSION	AI826623			
VERSION	AI826623.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 409)			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
COMMENT	Unpublished			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.			
	cDNA Library Preparation: M. Bento Soares, Ph.D.			
	CDNA Library Arrayed by: Greg Lennon, Ph.D.			
	DNA sequencing by: Washington University Genome Sequencing Center			
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/bbtp/image/image.html			
	Insert Length: 462			
	Seq primer: -40UP from Gibco.			
FEATURES	Location/Qualifiers			
source	1..409			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:2417395"			
	/sex="male"			
	/tissue_type="normal prostate"			
	/lab_host="DH10B"			
	/clone_id="NCI_CGAP_P122"			
	/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."			
BASE COUNT	112 a			
ORIGIN	94 c			
	80 g			
	123 t			
Alignment Scores:				
Pred. No.:	3,14e-56			
Score:	508.00			
Percent Similarity:	100.00%			
Best Local Similarity:	100.00%			
Query Match:	100.00%			
DB:	9			
	Gaps:			
	0			

	US-09-801-115B-2 (1--99) x A1826623 (1--409)
Oy	1 MetApsanValGlnProlysiIleYshIAArgProPheCyPheSerVallySGlyVHis 20
Db	367 ATGGATTAACGTGAAGCGGAAATAAACATCCGCCCTTCGTGCATTCACTGTGAAGAGCCAC 308
Oy	21 VallyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db	307 GTGAAGATGCTGGCGCTGGATATTATTCATCCTACTGTTAACACAGATTCAAGCTCATC 248
Oy	41 ValSerValLeuAlaLeuIleProGluThrThrThreuthValGIgylGIyValPhe 60
Db	247 GATATCTGTGGCACTGATATCACGAAAACACAACATTGACAGTGTGTGAGGAGGCTTT 188
Oy	61 AlaleuValThrAlaValCysCysLeuAlaAspGIyAlaLeuIleTYArgLysLeuLeu 80
Db	187 GCACCTGTGTGACGACGATATCTGTCTTGCCGACGGGCGCTTATTATTCGGAAGCTTCTG 128
Oy	81 PheaAnProSerGIyProTYrgInLYSLySProValHISgluLYSLySGlUValLeu 99
Db	127 TTCAATCCGACGCGTCTTACCAGAAAAACCTCTGATATAAAAAAGAAGTTTG 71
RESULT 8	
A1128804/c	LOCUS 423 bp mRNA linear EST 05-OCT-1998
DEFINITION	G994D08.61 Soares fetal heart NBH19W Homo sapiens cDNA clone
ACCESSION	IMAGE:1694391 3' "_mRNA_sequence."
VERSION	A1128804
KEYWORDS	A1128804.1 GI:3597318
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homniidae; Homo.
REFERENCE	1 (bases 1 to 423)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished
COMMENT	Contact: Robert Straubeberg, Ph.D. Email: cgapbs-f@mail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 382 Std Error: 0.00 Seq primer: -40ml3 fwd. RT from Amersham High quality sequence, stop: 413. Location/Qualifiers
FEATURES	1..423
source	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:1694391"
	/sex="unknown"
	/dev_stage="19 weeks"
	/lab_host="DH10B (ampicillin resistant)"
	/clone_lib="Soares fetal heart NBH19W"
	/note="Organ: heart; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st modified cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."
BASE COUNT	116 a 101 c 89 g 117 t
ORIGIN	
Alignment Scores:	

Pred. No.: 3.27e-56 Length: 423
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x A1128804 (1-423)

Qy 1 MetaspasVAlGInProLySleYsHleAArgProPhCySPheSeVallyGlyHis 20
 Db 353 ATGATTAACGTGCAGCCGAAATAAATCAATGCCCCCTTCTCTCAGTGTAAAGGCCAC 294
 Qy 21 VallysMetLeuAryLeuAspIleIleasnSerLeuValThrThyValPheMetLeuIle 40
 Db 293 GTGAAGATGCTGGCGCTGATATTATCACTCACTGGTAACAACAGTATTTCATCTATC 234
 Qy 41 ValSerValleuAlaLeuIleProGluThrThrThreuthrValGlyGlyValPhe 60
 Db 233 GTATCTGTGTGGCAGTATACCAAGAACCAACATTCAGTGTGGAGGGGTGTTT 174
 Qy 61 AlaleuValThrAlaValCySleuAlaAspGlyAlaLeuIleTyArgLyLeu 80
 Db 173 GCACCTTGACAGCAGTATGCTCTTCCGACGGGGCCCTTATTACCGAAGCTTCTG 114
 Qy 81 PheasnProSerGlyProTyGlnLySlyProValHisGluLySlyGluValLeu 99
 Db 113 TTCATCCAGCGGTCTTACCAAAAAGCCTGTGCATGAAAAAAGAAAGTTTG 57

RESULT 9 427 bp mRNA linear EST 06-JUN-1997
 LOCUS AA455042/c aad4a07.s1 Soares_NHMPu_s1 Homo sapiens cDNA clone IMAGE:812244
 DEFINITION 3', mRNA sequence.
 ACCESSION AA455042
 VERSION AA455042.1 GI:2177818
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 427)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

TITLE Contact: Wilson RK
 JOURNAL Washington University School of Medicine
 COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -41m3 fwd. ET from Amersham
 High quality sequence stop: 395.
 Location/Qualifiers

FEATURES

source

1. 427
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:6043155"
 /db_xref="taxon:9606"
 /clone="IMAGE:812244"
 /cissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares NHMPu_s1"
 /note="Organ: mixed (see below); Vector: pTTT3D-Pac
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI; Equal amounts of plasmid from three
 normalized libraries (melanocyte 2NBH, pregnant uterus

NbHPU, and fetal heart NbH19W) were mixed, and as circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

BASE COUNT 119 a 101 c 91 g 116 t
 ORIGIN

Alignment Scores:

Pred. No.: 3.31e-56 Length: 427
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AA455042 (1-427)

Qy 1 MetaspasVAlGInProLySleYsHleAArgProPhCySPheSeVallyGlyHis 20
 Db 356 ATGATTAACGTGCAGCCGAAATAAATCAATGCCCCCTTCTCTCAGTGTAAAGGCCAC 297
 Qy 21 VallysMetLeuAryLeuAspIleIleasnSerLeuValThrThyValPheMetLeuIle 40
 Db 296 GTGAAGATGCTGGCGCTGATATTATCACTCACTGGTAACAACAGTATTTCATCTATC 237
 Qy 41 ValSerValleuAlaLeuIleProGluThrThrThreuthrValGlyGlyValPhe 60
 Db 236 GTATCTGTGTGGCAGTATACCAAGAACCAACATTCAGTGTGGAGGGGTGTTT 177
 Qy 61 AlaleuValThrAlaValCySleuAlaAspGlyAlaLeuIleTyArgLyLeu 80
 Db 176 GCACCTTGACAGCAGTATGCTCTTCCGACGGGGCCCTTATTACCGAAGCTTCTG 117
 Qy 81 PheasnProSerGlyProTyGlnLySlyProValHisGluLySlyGluValLeu 99
 Db 116 TTCATCCAGCGGTCTTACCAAAAAGCCTGTGCATGAAAAAAGAAAGTTTG 60

RESULT 10 432 bp mRNA linear EST 16-OCT-1997
 LOCUS AA429945/c zw67f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781291
 DEFINITION 3', mRNA sequence.
 ACCESSION AA429945
 VERSION AA429945.1 GI:2113244
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

REFERENCE

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

AUTHORS

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

TITLE

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

JOURNAL

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

COMMENT

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

FEATURES

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
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 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

source

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

FEATURES

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
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 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

source

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 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
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 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

FEATURES

1 (bases 1 to 432)
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 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

source

1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished

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/db_xref="taxon:9606"
/clone="IMAGE:781291"
/sex="male"
/lab host="DH10B"
/notes="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGAGCGGCGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
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BASE COUNT 119 a 101 c 92 g 120 t

ORIGIN

Alignment Scores:

Pred. No.:	3,36e-56	Length:	432
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-801-115B-2 (1-99) x AA429945 (1-432)

QY 1 MetaspasmyValGlnProlysiLeuYshSArgProPheCySpheSerVallyGlyHis 20

DB 361 ATGGATACGCGCGCGGAAATAAACATCGCCCTTCTGCTTCACTGAGGAGGCGCAC 302

QY 21 VallySerMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

DB 301 GTGAGAGTCTGCGCGCTGGATATTATCACTCACTGTGAACAAGATTCATCTCATC 242

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

DB 241 GTATCTGTGTGGCAGTATCCAGAAACCAACATTCAGTGGTGGAGGGGTGTTT 182

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraArgLysLeuLeu 80

DB 181 GCATCTGTGACAGACAGATAGCTGTCTGCCGACGCGGCGCTTATTACCGGAACCTTCG 122

QY 81 PheAsnProSerGlyProTyrgInlySLysProValHisGluLysLysGluValLeu 99

DB 121 TTCATCCACGCGGCTCTTACCAAGAAAGCCCTGTGATGAAAAAAGAGTTTGG 65

RESULT 11

LOCUS A1078580 452 bp mRNA linear EST 10-AUG-1998

DEFINITION 3', mRNA sequence.

ACCESSION A1078580

VERSION A1078580.1 GI:3412988

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 410. Location/Qualifiers

FEATURES

source 1..452

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:167561"
/tissue type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab host="DH10B"
/clone lib="Soares_NhMpu_S1"
/notes="Organ: mixed (see below); Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH13W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
```

BASE COUNT 125 a 110 c 97 g 120 t

ORIGIN

Alignment Scores:

Pred. No.:	3,56e-56	Length:	452
Score:	508.00 <td>Matches:</td> <td>99</td>	Matches:	99
Percent Similarity:	100.00% <td>Conservative:</td> <td>0</td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0</td>	Mismatches:	0
Query Match:	100.00% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	9	Gaps:	0

US-09-801-115B-2 (1-99) x A1078580 (1-452)

QY 1 MetaspasmyValGlnProlysiLeuYshSArgProPheCySpheSerVallyGlyHis 20

DB 359 ATGGATACGCGCGCGGAAATAAACATCGCCCTTCTGCTTCACTGAGGAGGCGCAC 300

QY 21 VallySerMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

DB 299 GTGAGAGTCTGCGCGCTGGATATTATCACTCACTGTGAACAAGATTCATCTCATC 240

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

DB 239 GTATCTGTGTGGCAGTATCCAGAAACCAACATTCAGTGGTGGAGGGGTGTTT 180

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraArgLysLeuLeu 80

DB 179 GCATCTGTGACAGACAGATAGCTGTCTGCCGACGCGGCGCTTATTACCGGAACCTTCG 120

QY 81 PheAsnProSerGlyProTyrgInlySLysProValHisGluLysLysGluValLeu 99

DB 119 TTCATCCACGCGGCTCTTACCAAGAAAGCCCTGTGATGAAAAAAGAGTTTGG 63

RESULT 12

LOCUS A1743235 453 bp mRNA linear EST 20-DEC-1999

DEFINITION wg90a02.x1 Soares NSF P8.9W OT PA_P.S1 Homo sapiens cDNA clone IMAGE:2372330 3', mRNA sequence.

ACCESSION A1743235

VERSION A1743235.1 GI:5111523

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgaps-f@mail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

RESULT	13
BUS64679	
LOCUS	BUS64679
DEFINITION	BUS64679 466 bp mRNA linear EST 16-SEP-2002
ACCESSION	AGSNCOURT_10371072 NIH_MGC_141 Homo sapiens cDNA clone
VERSION	BUS64679.1
KEYWORDS	IMAGE:6602806 5' , mRNA sequence.
SOURCE	BUS64679.1 GI:22914979
ORGANISM	EST.
	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 466)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .

[illegible]

LOCUS BF109912 468 bp mRNA linear EST 20-OCT-2000
DEFINITION 7171F03.x1 Soares NSF_F8_9W_OT_PA.P.S1 Homo sapiens cDNA clone
IMAGE:3526805.3' similar to TR:09UI41 Q9UI41 CHEMOKINE-LIKE FACTOR
1. [1] ;, mRNA sequence.
ACCESSION BF109912
VERSION BF109912.1 GI:109393602
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 468)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-f@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40UP from Gibco.
FEATURES
source
1..468
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3526805"
/lab_host="DH10B"
/clone_lib="Soares_NSF_F8_9W_OT_PA.P.S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHP pool 1:
309384-310919, 323208-325895 Soares NBHP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NBHP-9W pool 1:
758280-760583, 772104-774407 Soares NBHP pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHP
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 127 a 116 c 102 g 123 t
ORIGIN
Alignment Scores:
Pred. No.: 3,72e-56 Length: 468
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-801-115B-2 (1-99) x BF109912 (1-468)

QY 1 MetAspAsnValGlnProlysilElySHsArgProPhCySpheSerVallySGlyHis 20
Db 362 ATGGATTAACCTGCAGCCGAAATAAACATCGCCCTTCCTGCTGCACTGGAAGGCCAC 303

QY 21 VallyMetLeuArgLeuAspIleleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 302 GTGAAGATGCTGGCGCTGATATTATCACTGATGTAACAAGATTCAATGCTATC 243

QY 41 ValSerValLeuValLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 242 GTATCTGTGTGGACATGACGAAACCAACCAATTGACAGTGTGAGGGGCTTTT 183

QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleYrArgVlyLeuLeu 80
Db 182 GCACCTGTGACAGCAGTATGCTGTCTTCCGACGGGGCCCTTATTATCCGGAAGCTTCTG 123

QY 81 PheAsnProSerGlyProTyrglnlylsySproValHisGluIylySGluValLeu 99
Db 122 TTCATCCACAGCGCTCTTACCGAAGAAAGCCGTGTCATGAAAAAGAGAGTTTG 66

RESULT 15
LOCUS BF399486/c 510 bp mRNA linear EST 27-NOV-2000
DEFINITION UI-R-CA1-bjb-b-12-0-UI.s1 UI-R-CA1 Rattus norvegicus cDNA clone
UI-R-CA1-bjb-b-12-0-UI 3', mRNA sequence.
ACCESSION BF399486
VERSION BF399486.1 GI:11384494
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 510)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE 8889548
PUBMED
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLVA=Yes.
FEATURES
source
1..510
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CA1-bjb-b-12-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CA1"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-CA1
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
'midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at rattest.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_SEQ=None found"

BASE COUNT 130 a 131 c 104 g 145 t
ORIGIN
Alignment Scores:
Pred. No.: 4.14e-56 Length: 510
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-801-115B-2 (1-99) x BF399486 (1-510)

QY 1 MetAspAsnValGlnProlysilElySHsArgProPhCySpheSerVallySGlyHis 20

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Db      371  ATGGATAACGTCAGCCGAAATAAAACATGCCCCCTTCTGCTTCAGTGTGAAAGGCCAC 312
Qy      21   ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db      311  GTGAGAGTGTGCGGCTGGATATTATCACTGACTGGTAAACAGATTTCATGCTCATC 252
Qy      41   ValSerValLeuAlaLeuIleProGluThrThrLeuThrValGlyGlyValPhe 60
Db      251  GTATCTGTGTGGACACTGATCCAGAAACCAACATTGACAGTTGGTGGAGGGGTGTTT 192
Qy      61   AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
Db      191  GCACTGTGACAGCAGATGCTGCTTGCCGACGGGGCCCTTATTATACCGGAAGCTTCTG 132
Qy      81   PheAsnProSerGlyProTyrGlnLysProValHisGluLysLysGluValLeu 99
Db      131  TTCATCCCGAGGGTCTTACCAAGAAAAAGCCTGTGCAATGAAAAAAGAGTTTGG 75

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Search completed: January 31, 2004, 05:25:28
 Job time : 2061 secs